GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: September 30, 2003, 16:35:33 ; Search time 414.636 Seconds
(without alignments)
12661.132 Million cell updates/sec

Title: US-09-856-681-3
Perfect score: 216
Sequence: 1 ccgccgcccgccccgcagag.....agcccaatgatgcgtgtaca 216

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rod:*
26: em_gss_phg:*
27: em_gss_vrl:*
28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	216	100.0	495	12	BM855120	BM855120 K-EST0137
	2	216	100.0	496	9	AV704776	AV704776 AV704776
	3	216	100.0	815	13	BU850016	BU850016 AGENCOURT
	4	216	100.0	862	13	BQ723018	BQ723018 AGENCOURT
	5	216	100.0	928	10	BE898612	BE898612 601681550
	6	216	100.0	1013	10	BE899378	BE899378 601681309
	7	215	99.5	494	14	N31401	N31401 yx67d08.r1
	8	212.8	98.5	6875	11	BC032619	BC032619 Homo sapi
	9	212	98.1	462	14	N25829	N25829 yx22d01.r1
	10	203.6	94.3	410	14	N46020	N46020 yy35a05.r1
	11	193.6	89.6	632	14	CB577257	CB577257 AMGNNUC:C
	12	193.6	89.6	711	14	CB246380	CB246380 UI-M-FI0-
	13	193.6	89.6	2411	14	CB605722	CB605722 AMGNNUC:M
c	14	178	82.4	291	10	BF702343	BF702343 MI-P-A2-a
	15	177.2	82.0	1183	12	BM546059	BM546059 AGENCOURT
c	16	166.4	77.0	364	9	AA729933	AA729933 nx40f11.s
	17	166.2	76.9	628	9	AA625166	AA625166 af67e09.r
	18	161	74.5	304	9	AA369179	AA369179 EST80573
	19	161	74.5	624	10	AW957071	AW957071 EST369141
	20	159.6	73.9	486	10	BF775045	BF775045 285089 MA
	21	159.6	73.9	598	9	AV593974	AV593974 AV593974
c	22	154	71.3	556	9	AA909230	AA909230 ol12h08.s
c	23	141.8	65.6	342	14	CB693654	CB693654 AMGNNUC:C
	24	135.6	62.8	895	12	BI819955	BI819955 603035314
	25	117.6	54.4	841	13	BU390763	BU390763 603511251
	26	117.6	54.4	841	13	BU394026	BU394026 603802267
c	27	110.6	51.2	1201	9	AL543312	AL543312 AL543312
	28	104.8	48.5	581	14	CB426060	CB426060 601199 MA
	29	104.8	48.5	852	10	BF306161	BF306161 601893009
	30	102.6	47.5	732	13	BQ180391	BQ180391 UI-M-EX0-
	31	99	45.8	543	10	BG698043	BG698043 602659189
	32	90.2	41.8	566	12	BJ060286	BJ060286 BJ060286
	33	89.4	41.4	409	14	W92871	W92871 zd92h03.r1
c	34	84.6	39.2	602	14	N22686	N22686 yx64c02.s1
	35	71.8	33.2	145	10	BG003350	BG003350 RC0-GN013
	36	62.8	29.1	829	12	BI824613	BI824613 603033546
	37	58.8	27.2	685	10	BE265000	BE265000 601193829
c	38	58.4	27.0	589	14	CB426401	CB426401 601583 MA
c	39	55	25.5	420	10	BE709445	BE709445 IL3-HT061
	40	55	25.5	708	14	CD356790	CD356790 AGENCOURT
	41	55	25.5	740	10	BG571342	BG571342 602592610
	42	55	25.5	792	10	BE543221	BE543221 601069213
	43	55	25.5	3405	11	BC004330	BC004330 Homo sapi
	44	51.8	24.0	483	14	CA875525	CA875525 K0941E11-
	45	51.8	24.0	499	14	CA873900	CA873900 K0928D02-

ALIGNMENTS

RESULT 1
BM855120
LOCUS BM855120 495 bp mRNA linear EST 06-MAR-2002
DEFINITION K-EST0137909 S22SNU16n1 Homo sapiens cDNA clone S22SNU16n1-150-D07 5', mRNA sequence.
ACCESSION BM855120
VERSION BM855120.1 GI:19211519
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 495)
AUTHORS Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R., Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and Kim,Y.S.
TITLE 21C Frontier Korean EST Project 2001
JOURNAL Unpublished
COMMENT Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr
Plate: 150 row: D column: 07
High quality sequence stop: 495.

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FEATURES             Location/Qualifiers
     source          1. .495
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="S22SNU16n1-150-D07"
                     /sex="F"
                     /tissue_type="Ascites"
                     /cell_type="Lymphoblast-like"
                     /cell_line="SNU-16"
                     /lab_host="DH10B"
                     /clone_lib="S22SNU16n1"
                     /note="Organ: Stomach; Vector: pT7T3-Pac; Site_1: EcoRI;
                     Site_2: NotI; The S22SNU16 library was contributed by the
                     Soares laboratory and it was constructed as described by
                     Bonaldo, M.F., Lennon, G. and Soares, M.B. (1996), Genome
                     Research 6(9): 791-806. RNA was prepared from harvested
                     cells of SNU-16 culture. SNU-16 was obtained from
                     Korean Cell Line Bank (KCLB). SNU-16 was established from
                     ascitic fluids of Korean patients by Park J.G. et al.
                     (1990), Cancer Res 50: 2773-2780."
BASE COUNT      107 a    169 c    134 g     85 t
ORIGIN

  Query Match             100.0%;  Score 216;  DB 12;  Length 495;
  Best Local Similarity   100.0%;  Pred. No. 9.8e-48;
  Matches  216;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CCGCCGCCCGCCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         39 CCGCCGCCCGCCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC 98

Qy         61 CAGGCCGTGACTGTCTCGAGGCAGCCCAGCCTCAACGCCTACAACTCACTGACAAGGTCG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         99 CAGGCCGTGACTGTCTCGAGGCAGCCCAGCCTCAACGCCTACAACTCACTGACAAGGTCG 158

Qy        121 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        159 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCC 218

Qy        181 CTTTCCACATCCATGAAGCCCAATGATGCGTGTACA 216
              ||||||||||||||||||||||||||||||||||||
Db        219 CTTTCCACATCCATGAAGCCCAATGATGCGTGTACA 254


RESULT 2
AV704776
LOCUS       AV704776                 496 bp    mRNA    linear   EST 09-OCT-2000
DEFINITION  AV704776 ADB Homo sapiens cDNA clone ADBBJC04 5', mRNA sequence.
ACCESSION   AV704776
VERSION     AV704776.1  GI:10722088
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 496)
  AUTHORS   Peng,Y., Song,H., Huang,Q., Huang,C., Gu,Y., Yang,Y., Gao,G., Xiao
            ,H., Xu,X., Li,N., Qian,B., Liu,F., Qu,J., Gao,X., Cheng,Z., Xu,Z.,
            Zeng,L., Xu,S., Gu,W., Tu,Y., Jia,J., Fu,G., Ren,S., Zhong,M., Lu
            ,G., Hu,R., Chen,J., Chen,Z. and Han,Z.
  TITLE     Homo sapiens cDNA ADB clones
  JOURNAL   Unpublished
COMMENT     Contact: Zeguang Han
            Chinese National Human Genome Center at Shanghai
            351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
            201203, P. R. China
            Tel: 86-21-50801919(ex.45)
            Fax: 86-21-50801922
            Email: hanzg@chgc.sh.cn
            This clone is available at CHGC in Shanghai.
FEATURES             Location/Qualifiers
     source          1. .496
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="ADBBJC04"
                     /tissue_type="Adrenal gland"
                     /dev_stage="Adult"
                     /lab_host="SOLR"
                     /clone_lib="ADB"
                     /note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2:
                     XhoI"
BASE COUNT      107 a    178 c    131 g     80 t
ORIGIN

  Query Match             100.0%;  Score 216;  DB 9;  Length 496;
  Best Local Similarity   100.0%;  Pred. No. 9.8e-48;
  Matches  216;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CCGCCGCCCGCCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CCGCCGCCCGCCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC 240

Qy         61 CAGGCCGTGACTGTCTCGAGGCAGCCCAGCCTCAACGCCTACAACTCACTGACAAGGTCG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CAGGCCGTGACTGTCTCGAGGCAGCCCAGCCTCAACGCCTACAACTCACTGACAAGGTCG 300

Qy        121 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCC 360

Qy        181 CTTTCCACATCCATGAAGCCCAATGATGCGTGTACA 216
              ||||||||||||||||||||||||||||||||||||
Db        361 CTTTCCACATCCATGAAGCCCAATGATGCGTGTACA 396


RESULT 3
BU850016
LOCUS       BU850016                 815 bp    mRNA    linear   EST 16-OCT-2002
DEFINITION  AGENCOURT_10438272 NIH_MGC_109 Homo sapiens cDNA clone
            IMAGE:6598770 5', mRNA sequence.
ACCESSION   BU850016
VERSION     BU850016.1  GI:24034979
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 815)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
             cDNA Library Preparation: Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM2832  row: b  column: 18
            High quality sequence stop: 700.
FEATURES             Location/Qualifiers
     source          1. .815
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:6598770"
                     /tissue_type="teratocarcinoma, cell line"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_109"
                     /note="Organ: ovary; Vector: pOTB7; Site_1: EcoRI; Site_2:
                     XhoI; cDNA made by oligo-dT priming.  Directionally cloned
                     into EcoRI/XhoI sites using the following 5' adaptor:
```

GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."
BASE COUNT 236 a 271 c 172 g 136 t
ORIGIN

Query Match 100.0%; Score 216; DB 13; Length 815;
Best Local Similarity 100.0%; Pred. No. 1.2e-47;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 CCGCCGCCCGCCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         96 CCGCCGCCCGCCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC 155

Qy         61 CAGGCCGTGACTGTCTCGAGGCAGCCCAGCCTCAACGCCTACAACTCACTGACAAGGTCG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        156 CAGGCCGTGACTGTCTCGAGGCAGCCCAGCCTCAACGCCTACAACTCACTGACAAGGTCG 215

Qy        121 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        216 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCC 275

Qy        181 CTTTCCACATCCATGAAGCCCAATGATGCGTGTACA 216
              ||||||||||||||||||||||||||||||||||||
Db        276 CTTTCCACATCCATGAAGCCCAATGATGCGTGTACA 311
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RESULT 4
BQ723018
LOCUS BQ723018 862 bp mRNA linear EST 16-JUL-2002
DEFINITION AGENCOURT_8099701 Lupski_sympathetic_trunk Homo sapiens cDNA clone IMAGE:6190272 5', mRNA sequence.
ACCESSION BQ723018
VERSION BQ723018.1 GI:21861915
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 862)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. James R. Lupski
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLAM13588 row: n column: 01
High quality sequence stop: 592.
FEATURES Location/Qualifiers
source 1. .862
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6190272"
/sex="male"
/tissue_type="sympathetic trunk"
/dev_stage="adult, 16 yr"
/lab_host="DH10B"
/clone_lib="Lupski_sympathetic_trunk"
/note="Vector: pCMV-SPORT6 (Life Technologies); Site_1: NotI; Site_2: SalI; cDNA made by oligo-dT priming. Directionally cloned using the following adaptors: 5'-TCGACCCACGCGTCCG-3' and 5'-GACTAGTTCTAGATCGCGAGCGGCCGCCCT(15)-3'. Size selected > 1 kb for average insert length 1.9 kb. This is a primary library, non-amplified. Library constructed by Life Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor College of Medicine); available through Life Technologies."
BASE COUNT 208 a 307 c 207 g 140 t
ORIGIN

Query Match 100.0%; Score 216; DB 13; Length 862;
Best Local Similarity 100.0%; Pred. No. 1.2e-47;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 CCGCCGCCCGCCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC 60
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Db        269 CCGCCGCCCGCCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC 328

Qy         61 CAGGCCGTGACTGTCTCGAGGCAGCCCAGCCTCAACGCCTACAACTCACTGACAAGGTCG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        329 CAGGCCGTGACTGTCTCGAGGCAGCCCAGCCTCAACGCCTACAACTCACTGACAAGGTCG 388

Qy        121 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        389 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCC 448

Qy        181 CTTTCCACATCCATGAAGCCCAATGATGCGTGTACA 216
              ||||||||||||||||||||||||||||||||||||
Db        449 CTTTCCACATCCATGAAGCCCAATGATGCGTGTACA 484
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RESULT 5
BE898612
LOCUS BE898612 928 bp mRNA linear EST 29-SEP-2000
DEFINITION 601681550F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3951685 5', mRNA sequence.
ACCESSION BE898612
VERSION BE898612.1 GI:10365266
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 928)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCM820 row: c column: 14
High quality sequence stop: 794.
FEATURES Location/Qualifiers
source 1. .928
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3951685"
/tissue_type="adenocarcinoma cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_9"
/note="Organ: ovary; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
BASE COUNT 245 a 314 c 215 g 154 t
ORIGIN

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  Query Match           100.0%;  Score 216;  DB 10;  Length 928;
  Best Local Similarity  100.0%;  Pred. No. 1.2e-47;
  Matches  216;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CCGCCGCCCGCCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        243 CCGCCGCCCGCCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC 302

Qy         61 CAGGCCGTGACTGTCTCGAGGCAGCCCAGCCTCAACGCCTACAACTCACTGACAAGGTCG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        303 CAGGCCGTGACTGTCTCGAGGCAGCCCAGCCTCAACGCCTACAACTCACTGACAAGGTCG 362

Qy        121 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        363 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCC 422

Qy        181 CTTTCCACATCCATGAAGCCCAATGATGCGTGTACA 216
              ||||||||||||||||||||||||||||||||||||
Db        423 CTTTCCACATCCATGAAGCCCAATGATGCGTGTACA 458


RESULT 6
BE899378
LOCUS       BE899378               1013 bp    mRNA    linear   EST 29-SEP-2000
DEFINITION  601681309F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3951266 5',
            mRNA sequence.
ACCESSION   BE899378
VERSION     BE899378.1  GI:10367019
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1013)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: DCTD/DTP
             cDNA Library Preparation: Ling Hong/Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
            Plate: LLCM819  row: b  column: 03
            High quality sequence start: 30
            High quality sequence stop: 828.
FEATURES             Location/Qualifiers
     source          1. .1013
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:3951266"
                     /tissue_type="adenocarcinoma cell line"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_9"
                     /note="Organ: ovary; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming.  Directionally
                     cloned into EcoRI/XhoI sites using the following 5'
                     adaptor: GGCACGAG(G).  Size-selected >500bp for average
                     insert size 1.8kb.  Library constructed by Ling Hong in
                     the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using  ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies)."
BASE COUNT      270 a    322 c    263 g    158 t
ORIGIN

  Query Match           100.0%;  Score 216;  DB 10;  Length 1013;
  Best Local Similarity  100.0%;  Pred. No. 1.2e-47;
  Matches  216;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CCGCCGCCCGCCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        292 CCGCCGCCCGCCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC 351

Qy         61 CAGGCCGTGACTGTCTCGAGGCAGCCCAGCCTCAACGCCTACAACTCACTGACAAGGTCG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        352 CAGGCCGTGACTGTCTCGAGGCAGCCCAGCCTCAACGCCTACAACTCACTGACAAGGTCG 411

Qy        121 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        412 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCC 471

Qy        181 CTTTCCACATCCATGAAGCCCAATGATGCGTGTACA 216
              ||||||||||||||||||||||||||||||||||||
Db        472 CTTTCCACATCCATGAAGCCCAATGATGCGTGTACA 507


RESULT 7
N31401
LOCUS       N31401                 494 bp    mRNA    linear   EST 10-JAN-1996
DEFINITION  yx67d08.r1 Soares melanocyte 2NbHM Homo sapiens cDNA clone
            IMAGE:266799 5', mRNA sequence.
ACCESSION   N31401
VERSION     N31401.1  GI:1151800
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 494)
  AUTHORS   Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman
            ,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J.,
            Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston
            ,R., Williamson,A., Wohldmann,P. and Wilson,R.
  TITLE     The WashU-Merck EST Project
  JOURNAL   Unpublished
COMMENT     Contact: Wilson RK
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            High quality sequence stops: 464
            Source: IMAGE Consortium, LLNL
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Seq primer: T7
            High quality sequence stop: 464.
FEATURES             Location/Qualifiers
     source          1. .494
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="GDB:3876441"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:266799"
                     /sex="Male"
                     /tissue_type="melanocyte"
                     /lab_host="DH10B (ampicillin resistant)"
                     /clone_lib="Soares melanocyte 2NbHM"
                     /note="Vector: pT7T3D (Pharmacia) with a modified
                     polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
                     was primed with a Not I - oligo(dT) primer [5'
                     TGTTACCAATCTGAAGTGGGAGCGGCCGCAGTTTTTTTTTTTTTTTTTT 3'],
                     double-stranded cDNA was size selected, ligated to Eco RI
                     adapters (Pharmacia), digested with Not I and cloned into
                     the Not I and Eco RI sites of a modified pT7T3 vector
                     (Pharmacia). Library constructed by Bento Soares and
                     M.Fatima Bonaldo. RNA from normal foreskin melanocytes
                     (FS374) was kindly provided by Dr. Anthony P. Albino."
BASE COUNT      110 a    165 c    131 g     83 t      5 others
ORIGIN

  Query Match           99.5%;  Score 215;  DB 14;  Length 494;
```

```
  Best Local Similarity   99.5%;  Pred. No. 1.8e-47;
  Matches  215;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 CCGCCGCCCGCCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db         60 CCGCCGCCCGCCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGNC 119

Qy         61 CAGGCCGTGACTGTCTCGAGGCAGCCCAGCCTCAACGCCTACAACTCACTGACAAGGTCG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        120 CAGGCCGTGACTGTCTCGAGGCAGCCCAGCCTCAACGCCTACAACTCACTGACAAGGTCG 179

Qy        121 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        180 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCC 239

Qy        181 CTTTCCACATCCATGAAGCCCAATGATGCGTGTACA 216
              ||||||||||||||||||||||||||||||||||||
Db        240 CTTTCCACATCCATGAAGCCCAATGATGCGTGTACA 275


RESULT 8
BC032619
LOCUS       BC032619               6875 bp    mRNA    linear   HTC 04-MAR-2003
DEFINITION  Homo sapiens, similar to sema domain, transmembrane domain (TM),
            and cytoplasmic domain, (semaphorin) 6A, clone IMAGE:5578066, mRNA.
ACCESSION   BC032619
VERSION     BC032619.1  GI:22749800
KEYWORDS    HTC.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 6875)
  AUTHORS   Strausberg,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (06-JUN-2002) National Institutes of Health, Mammalian
            Gene Collection (MGC), Cancer Genomics Office, National Cancer
            Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
            USA
  REMARK    NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT     Contact: MGC help desk
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC/DCTD/DTP
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: National Institutes of Health Intramural
            Sequencing Center (NISC),
            Gaithersburg, Maryland;
            Web site: http://www.nisc.nih.gov/
            Contact: nisc_mgc@nhgri.nih.gov
            Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
            Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
            Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,
            Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,
            Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D.,McCloskey,J.C.,
            McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
            Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
            Young,A., Zhang,L.-H. and Green,E.D.

            Clone distribution: MGC clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
            Series: IRAK Plate: 69 Row: o Column: 4
            This clone was selected for full length sequencing because it
            passed the following selection criteria: matched mRNA gi: 11991659
            This clone has the following problem: retained intron.
FEATURES             Location/Qualifiers
     source          1. .6875
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5578066"
                     /tissue_type="Skin, melanotic melanoma."
                     /clone_lib="NIH_MGC_72"
                     /lab_host="DH10B"
                     /note="Vector: pCMV-SPORT6"
BASE COUNT     1784 a   1795 c   1592 g   1704 t
ORIGIN

  Query Match           98.5%;  Score 212.8;  DB 11;  Length 6875;
  Best Local Similarity   99.1%;  Pred. No. 1.7e-46;
  Matches  214;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 CCGCCGCCCGCCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC 60
              |||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db       3666 CCGCCGCCCGCCCCGCAGAGGGTGGACTCCATCCCGGTGCACAGCTCCCAGCCATCTGGC 3725

Qy         61 CAGGCCGTGACTGTCTCGAGGCAGCCCAGCCTCAACGCCTACAACTCACTGACAAGGTCG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3726 CAGGCCGTGACTGTCTCGAGGCAGCCCAGCCTCAACGCCTACAACTCACTGACAAGGTCG 3785

Qy        121 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCC 180
              |||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3786 GGGCTGTAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCC 3845

Qy        181 CTTTCCACATCCATGAAGCCCAATGATGCGTGTACA 216
              ||||||||||||||||||||||||||||||||||||
Db       3846 CTTTCCACATCCATGAAGCCCAATGATGCGTGTACA 3881


RESULT 9
N25829
LOCUS       N25829                 462 bp    mRNA    linear   EST 29-DEC-1995
DEFINITION  yx22d01.r1 Soares melanocyte 2NbHM Homo sapiens cDNA clone
            IMAGE:262465 5', mRNA sequence.
ACCESSION   N25829
VERSION     N25829.1  GI:1140177
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 462)
  AUTHORS   Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman
            ,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J.,
            Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston
            ,R., Williamson,A., Wohldmann,P. and Wilson,R.
  TITLE     The WashU-Merck EST Project
  JOURNAL   Unpublished
COMMENT     Contact: Wilson RK
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            High quality sequence stops: 360
            Source: IMAGE Consortium, LLNL
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Insert Length: 1117   Std Error: 0.00
            Seq primer: T7
            High quality sequence stop: 360.
FEATURES             Location/Qualifiers
     source          1. .462
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="GDB:3872107"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:262465"
                     /sex="Male"
                     /tissue_type="melanocyte"
                     /lab_host="DH10B (ampicillin resistant)"
                     /clone_lib="Soares melanocyte 2NbHM"
                     /note="Vector: pT7T3D (Pharmacia) with a modified
                     polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
                     was primed with a Not I - oligo(dT) primer [5'
                     TGTTACCAATCTGAAGTGGGAGCGGCCGCAGTTTTTTTTTTTTTTTTT 3'],
```

double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library constructed by Bento Soares and M.Fatima Bonaldo. RNA from normal foreskin melanocytes (FS374) was kindly provided by Dr. Anthony P. Albino."
BASE COUNT 111 a 167 c 103 g 77 t 4 others
ORIGIN

Query Match 98.1%; Score 212; DB 14; Length 462;
Best Local Similarity 98.1%; Pred. No. 1.1e-46;
Matches 212; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

```
Qy          1 CCGCCGCCCGCCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        238 CCGCCGCCCGCCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC 297

Qy         61 CAGGCCGTGACTGTCTCGAGGCAGCCCAGCCTCAACGCCTACAACTCACTGACAAGGTCG 120
              |||||||||||||||||||||||||||||||| |||||| ||||||||||||||||
Db        298 CAGGCCGTGACTGTCTCGAGGCAGCCCAGCCTCAACGNCTACAANTCACTGACAAGGTCG 357

Qy        121 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCC 180
              |||||||||||||||||||||||||||||||||||||||||||||||| |||| ||||
Db        358 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCNTTTGNTCCC 417

Qy        181 CTTTCCACATCCATGAAGCCCAATGATGCGTGTACA 216
              |||||||||||||||||||||||||||||||||||
Db        418 CTTTCCACATCCATGAAGCCCAATGATGCGTGTACA 453
```

RESULT 10
N46020
LOCUS N46020 410 bp mRNA linear EST 14-FEB-1996
DEFINITION yy35a05.r1 Soares melanocyte 2NbHM Homo sapiens cDNA clone IMAGE:273200 5', mRNA sequence.
ACCESSION N46020
VERSION N46020.1 GI:1187186
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 410)
AUTHORS Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and Wilson,R.
TITLE The WashU-Merck EST Project
JOURNAL Unpublished
COMMENT Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: T7
High quality sequence stop: 329.
FEATURES Location/Qualifiers
source 1. .410
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:3882842"
/db_xref="taxon:9606"
/clone="IMAGE:273200"
/sex="Male"
/tissue_type="melanocyte"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares melanocyte 2NbHM"
/note="Vector: pT7T3D (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTACCAATCTGAAGTGGGAGCGGCCGCAGTTTTTTTTTTTTTTTTTT 3'], double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT7T3 vector (Pharmacia). Library constructed by Bento Soares and M.Fatima Bonaldo. RNA from normal foreskin melanocytes (FS374) was kindly provided by Dr. Anthony P. Albino."
BASE COUNT 99 a 143 c 101 g 62 t 5 others
ORIGIN

Query Match 94.3%; Score 203.6; DB 14; Length 410;
Best Local Similarity 98.1%; Pred. No. 1.9e-44;
Matches 206; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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Qy          7 CCCGCCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGCCAGGCC 66
              || |||  ||||||||||||||||||||||||||||||||||||||||||||||||||
Db         78 CCGCCCCACCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGCCAGGCC 137

Qy         67 GTGACTGTCTCGAGGCAGCCCAGCCTCAACGCCTACAACTCACTGACAAGGTCGGGGGCTG 126
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        138 GTGACTGTCTCGAGGCAGCCCAGCCTCAACGCCTACAACTCACTGACAAGGTCGGGGCTG 197

Qy        127 AAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCCCTTTCC 186
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        198 AAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCCCTTTCC 257

Qy        187 ACATCCATGAAGCCCAATGATGCGTGTACA 216
              |||||||||||||||||||||||||||||
Db        258 ACATCCATGAAGCCCAATGATGCGTGTACA 287
```

RESULT 11
CB577257
LOCUS CB577257 632 bp mRNA linear EST 03-APR-2003
DEFINITION AMGNNUC:CDRG1-00015-G10-A cdrg1 (10898) Rattus norvegicus cDNA clone cdrg1-00015-g10 5', mRNA sequence.
ACCESSION CB577257
VERSION CB577257.1 GI:29521298
KEYWORDS EST.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
REFERENCE 1 (bases 1 to 632)
AUTHORS Amgen EST Program.
TITLE Amgen Rat EST Program
JOURNAL Unpublished
COMMENT Contact: Dan Fitzpatrick
Amgen, Inc
One Amgen Center Drive, Thousand Oaks, CA 91320-1799, USA
Tel: 805 447-4881
Plate: 00015 row: g column: 10.
FEATURES Location/Qualifiers
source 1. .632
/organism="Rattus norvegicus"
/mol_type="mRNA"
/db_xref="taxon:10116"
/clone="cdrg1-00015-g10"
/tissue_type="Chung Model Ipsilate"
/clone_lib="cdrg1 (10898)"
/note="Vector: pSPORT1; Chung Model Rat DRG Left L5/L6"
BASE COUNT 155 a 213 c 151 g 113 t
ORIGIN

Query Match 89.6%; Score 193.6; DB 14; Length 632;
Best Local Similarity 93.5%; Pred. No. 1.1e-41;
Matches 202; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

```
Qy          1 CCGCCGCCCGCCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC 60
              || || |||||||||||||||||||||| ||||||||||||||| ||||||| ||||||
Db         20 CCACCTCCCGCCCCGCAGAGGGTGGACTCTATCCAGGTGCACAGCCCCCAGCCCTCTGGC 79
```

```
Qy          61 CAGGCCGTGACTGTCTCGAGGCAGCCCAGCCTCAACGCCTACAACTCACTGACAAGGTCG 120
               ||||||||||||||| |||||||||||||||||||| |||||||||||||||||| ||||||
Db          80 CAGGCCGTGACTGTTTCGAGGCAGCCCAGCCTCAATGCCTACAACTCACTGACGAGGTCG 139

Qy         121 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCC 180
               |||||||||| || |||||||||||||| || |||||||||||||| |||||||| |||
Db         140 GGGCTGAAGCGCACCCCCTCGCTAAAGCCAGATGTACCCCCCAAACCTTCCTTTGCCCCC 199

Qy         181 CTTTCCACATCCATGAAGCCCAATGATGCGTGTACA 216
               |||||||||||||||||||||||||||||||||||
Db         200 CTTTCCACATCCATGAAGCCCAATGATGCGTGTACA 235


RESULT 12
CB246380
LOCUS       CB246380                711 bp    mRNA    linear   EST 12-FEB-2003
DEFINITION  UI-M-FI0-cdw-i-10-0-UI.r1 NIH_BMAP_FI0 Mus musculus cDNA clone
            IMAGE: 6835379 5', mRNA sequence.
ACCESSION   CB246380
VERSION     CB246380.1  GI:28368024
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 711)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Jim Lin, University of Iowa
             cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
             cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
             DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
             Clone Distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
             This clone was contributed by the Brain Molecular Anatomy Project
            (BMAP)
             The following repetitive elements were found in this cDNA
            sequence: 563-665, >(CA)n#Simple_repeat
            Seq primer: pYX-5.
FEATURES             Location/Qualifiers
     source          1. .711
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="C57BL/6"
                     /db_xref="taxon:10090"
                     /clone="IMAGE: 6835379"
                     /tissue_type="whole brain"
                     /dev_stage="embryo 12.5dpc"
                     /lab_host="DH10B (T1 phage resistant)"
                     /clone_lib="NIH_BMAP_FI0"
                     /note="Organ: Brain; Vector: pYX- Asc; Site_1: EcoR I;
                     Site_2: Not I; The library was constructed according
                     Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
                     1996. Denatured RNA was size fractionated on a 1% agarose
                     gel.First strand cDNA synthesis was primed with oligo-dT
                     primer containing a Not I site. Double strand cDNA was
                     size selected according to mRNA size fraction, ligated
                     with EcoR I adaptor, digested with NotI and then cloned
                     directionally into pYX-Asc vector. The library tag
                     sequence located between the Not I site and the polyA tail
                     is CAGCCACGAC. This library was created for the University
                     Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
                     Developing Mouse Nervous System', supported by National
                     Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,
                     program coordinator."
BASE COUNT      189 a    255 c    141 g    125 t      1 others
ORIGIN

  Query Match             89.6%;  Score 193.6;  DB 14;  Length 711;
  Best Local Similarity   93.5%;  Pred. No. 1.1e-41;
  Matches  202;  Conservative    0;  Mismatches   14;  Indels    0;  Gaps    0;

Qy           1 CCGCCGCCCGCCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC 60
               || || |||||||||||| |||||||||| |||||||||||||||||||||||| ||||||
Db           2 CCACCCCCCGCCCCGCAGCGGGTGGACTCTATCCAGGTGCACAGCTCCCAGCCCTCTGGC 61

Qy          61 CAGGCCGTGACTGTCTCGAGGCAGCCCAGCCTCAACGCCTACAACTCACTGACAAGGTCG 120
               |||||||||||||| |||||||||||||||||||| |||||||||||||||||| ||||||
Db          62 CAGGCCGTGACTGTTTCGAGGCAGCCCAGCCTCAATGCCTACAACTCACTGACGAGGTCG 121

Qy         121 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCC 180
               |||||||||| || |||||||||||||| || |||||||||||||| |||||||||||
Db         122 GGGCTGAAGCGCACCCCCTCGCTAAAGCCAGATGTACCCCCCAAACCTTCCTTTGCTCCC 181

Qy         181 CTTTCCACATCCATGAAGCCCAATGATGCGTGTACA 216
               |||||||||||||||||||||||||||||| ||||||
Db         182 CTTTCCACATCCATGAAGCCCAATGATGCATGTACA 217


RESULT 13
CB605722
LOCUS       CB605722                2411 bp    mRNA    linear   EST 16-MAY-2003
DEFINITION  AMGNNUC:MRPE3-00075-D4-WY placenta embryo D17 (10379) Rattus
            norvegicus cDNA clone mrpe3-00075-d4, mRNA sequence.
ACCESSION   CB605722
VERSION     CB605722.1  GI:29545334
KEYWORDS    EST.
SOURCE      Rattus norvegicus (Norway rat)
  ORGANISM  Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.
REFERENCE   1  (bases 1 to 2411)
  AUTHORS   Amgen EST Program.
  TITLE     Amgen Rat EST Program
  JOURNAL   Unpublished
COMMENT     Contact: Dan Fitzpatrick
            Amgen, Inc
            One Amgen Center Drive, Thousand Oaks, CA 91320-1799, USA
            Tel: 805 447-4881
            Plate: 00075  row: d  column: 4.
FEATURES             Location/Qualifiers
     source          1. .2411
                     /organism="Rattus norvegicus"
                     /mol_type="mRNA"
                     /db_xref="taxon:10116"
                     /clone="mrpe3-00075-d4"
                     /tissue_type="placenta embryo"
                     /clone_lib="placenta embryo D17 (10379)"
                     /note="Vector: pSPORT1; placenta embryo D17"
BASE COUNT      658 a    689 c    557 g    505 t      2 others
ORIGIN

  Query Match             89.6%;  Score 193.6;  DB 14;  Length 2411;
  Best Local Similarity   93.5%;  Pred. No. 1.7e-41;
  Matches  202;  Conservative    0;  Mismatches   14;  Indels    0;  Gaps    0;

Qy           1 CCGCCGCCCGCCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC 60
               || || |||||||||||||||||||| |||||||||||||||| ||||||| ||||||
Db        1340 CCACCTCCCGCCCCGCAGAGGGTGGACTCTATCCAGGTGCACAGCCCCCAGCCCTCTGGC 1399

Qy          61 CAGGCCGTGACTGTCTCGAGGCAGCCCAGCCTCAACGCCTACAACTCACTGACAAGGTCG 120
               |||||||||||||| |||||||||||||||||||| |||||||||||||||||| ||||||
Db        1400 CAGGCCGTGACTGTTTCGAGGCAGCCCAGCCTCAATGCCTACAACTCACTGACGAGGTCG 1459

Qy         121 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCC 180
               |||||||||| || |||||||||||||| || |||||||||||||| |||||||| |||
Db        1460 GGGCTGAAGCGCACCCCCTCGCTAAAGCCAGATGTACCCCCCAAACCTTCCTTTGCCCCC 1519

Qy         181 CTTTCCACATCCATGAAGCCCAATGATGCGTGTACA 216
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Db        1520 CTTTCCACATCCATGAAGCCCAATGATGCGTGTACA 1555
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RESULT 14
BF702343/c
LOCUS       BF702343                291 bp    mRNA    linear   EST 22-DEC-2000
DEFINITION  MI-P-A2-aas-a-02-1-UM.s1 MI-P-A2 Sus scrofa cDNA clone
            MI-P-A2-aas-a-02-1-UM 3', mRNA sequence.
ACCESSION   BF702343
VERSION     BF702343.1  GI:11987751
KEYWORDS    EST.
SOURCE      Sus scrofa (pig)
  ORGANISM  Sus scrofa
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE   1  (bases 1 to 291)
  AUTHORS   Bonaldo,M.F., Lennon,G. and Soares,M.B.
  TITLE     Normalization and subtraction: two approaches to facilitate gene
            discovery
  JOURNAL   Genome Res. 6 (9), 791-806 (1996)
  MEDLINE   97044477
   PUBMED   8889548
COMMENT     Contact: Tuggle CK
            Molecular Genetics Laboratory, Department of Animal Science
            Iowa State University
            201 Kildee Hall, Ames, IA 50011-3150, USA
            Tel: 5152944252
            Fax: 5152942401
            Email: cktuggle@iastate.edu
            Oligo-dT track not found, Not I site shown in beginning of sequence
            is likely internal to the message. cDNA Library Preparation: RJ
            Woods, JA Green, RS Prather S142 Animal Science Research Center,
            Department of Animal Science, University of Missouri-Columbia,
            65211 Clone distribution: clones will be available through Research
            Genetics (www.resgen.com)
            Seq primer: M13 Forward
            POLYA=No.
FEATURES             Location/Qualifiers
     source          1. .291
                     /organism="Sus scrofa"
                     /mol_type="mRNA"
                     /strain="crossbreed"
                     /db_xref="taxon:9823"
                     /clone="MI-P-A2-aas-a-02-1-UM"
                     /lab_host="DH10B (Life Technologies)"
                     /clone_lib="MI-P-A2"
                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                     polylinker; Site_1: Not I; Site_2: EcoRI; The MI-P-A2
                     library is derived from anterior pituitary at estrus day
                     5.  For a detailed description of the  library from which
                     this clone was derived, please visit our web site at
                     http://pigest.genome.iastate.edu/.
                     TAG_SEQ=None found"
BASE COUNT       45 a     84 c    100 g     61 t      1 others
ORIGIN

  Query Match             82.4%;  Score 178;  DB 10;  Length 291;
  Best Local Similarity   90.5%;  Pred. No. 1.3e-37;
  Matches  190;  Conservative    0;  Mismatches   20;  Indels    0;  Gaps    0;

Qy          7 CCCGCCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGCCAGGCC 66
              |||   | ||||||||||||||||||||||||||||||||| ||||| ||||||||||
Db        287 CCCCTTCGGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCGCAGCCCTCTGGCCAGGCC 228

Qy         67 GTGACTGTCTCGAGGCAGCCCAGCCTCAACGCCTACAACTCACTGACAAGGTCGGGGGCTG 126
              |||||||| |||||||||| |||||||| ||||||||||||||||| ||| ||||||||
Db        227 GTGACTGTTTCGAGGCAGCCAAGCCTCAATGCCTACAACTCACTGACCAGGGCGGGGCTG 168

Qy        127 AAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCCCTTTCC 186
              || || || || |||||||||||||||||| ||||| ||||| |||||||| |||||||||
Db        167 AAACGCACCCCTTCGCTAAAGCCGGACGTGCCCCCGAAACCTTCCTTTGCCCCCCTTTCC 108

Qy        187 ACATCCATGAAGCCCAATGATGCGTGTACA 216
              |||||||||||||||||||| |||||||||
Db        107 ACATCCATGAAGCCCAATGACGCGTGTACA 78


RESULT 15
BM546059
LOCUS       BM546059                1183 bp    mRNA    linear   EST 20-FEB-2002
DEFINITION  AGENCOURT_6497880 NIH_MGC_125 Homo sapiens cDNA clone IMAGE:5588479
            5', mRNA sequence.
ACCESSION   BM546059
VERSION     BM546059.1  GI:18778712
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1183)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Invitrogen
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM12359  row: k  column: 08
            High quality sequence stop: 725.
FEATURES             Location/Qualifiers
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                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5588479"
                     /lab_host="DH10B"
                     /clone_lib="NIH_MGC_125"
                     /note="Organ: ovary (pool of 3); Vector: pCMV-SPORT6;
                     Site_1: EcoRV (destroyed); Site_2: NotI; RNA source pool
                     of three ovaries, from females ranging in age from 38 to
                     49 yo. Library is oligo-dT primed and directionally cloned
                     (EcoRV site is destroyed upon cloning). Average insert
                     size 2.1 kb, insert size range 1-3.5 kb. Library is
                     normalized and enriched for full-length clones and was
                     constructed by C. Gruber (Invitrogen). Research Genetics
                     tracking code 036."
BASE COUNT      284 a    428 c    309 g    161 t      1 others
ORIGIN

  Query Match             82.0%;  Score 177.2;  DB 12;  Length 1183;
  Best Local Similarity   97.2%;  Pred. No. 3.3e-37;
  Matches  212;  Conservative    0;  Mismatches    3;  Indels    3;  Gaps    3;

Qy          1 CCGCCGCCCGCCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        741 CCGCCGCCCGCCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC 800

Qy         61 CAGGCCGTGACTGTCTCGAGGCAGCCCAGCCTCAACGCCTACAACTCACTGACAAGGTC- 119
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Db        801 CAGGCCGTGACTGTCTCGAGGCAGCCCAGCCTCAACGCCTACAACTCACTGACAAAGTCG 860

Qy        120 GGGGCTGAAGCGTACG-CCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTC 178
              |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db        861 GGGGCTGAAGCGTACGCCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTC 920

Qy        179 CCCTTTCCACATCCATG-AAGCCCAATGATGCGTGTAC 215
              |||||| |||||||||| |||||| ||||||||||||
Db        921 CCCTTTTCACATCCATGAAAGCCCCATGATGCGTGTAC 958


Search completed: September 30, 2003, 22:02:15
Job time : 420.636 secs
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: September 30, 2003, 16:34:33 ; Search time 773.266 Seconds
(without alignments)
11427.482 Million cell updates/sec

Title: US-09-856-681-3
Perfect score: 216
Sequence: 1 ccgccgcccgccccgcagag.....agcccaatgatgcgtgtaca 216

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 20454813386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
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6: gb_pat:*
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8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
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24: em_ph:*
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33: em_htg_mus:*
34: em_htg_pln:*
35: em_htg_rod:*
36: em_htg_mam:*
37: em_htg_vrt:*
38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
1		216	100.0	216	6	AX026743	AX026743 Sequence
2		216	100.0	2123	6	BD155987	BD155987 Primer fo
3		216	100.0	2123	9	AK027439	AK027439 Homo sapi
4		216	100.0	2227	6	BD127394	BD127394 Primer fo
5		216	100.0	2227	9	AK074975	AK074975 Homo sapi
6		216	100.0	2293	6	BD157826	BD157826 Primer fo
7		216	100.0	2293	9	AK027471	AK027471 Homo sapi
8		216	100.0	2306	6	BD159853	BD159853 Primer fo
9		216	100.0	2306	9	AK027654	AK027654 Homo sapi
10		216	100.0	3041	6	BD159617	BD159617 Primer fo
11		216	100.0	3041	9	AK027501	AK027501 Homo sapi
12		216	100.0	3093	6	AX026741	AX026741 Sequence
13		216	100.0	3550	6	AX099520	AX099520 Sequence
14		216	100.0	3634	9	AK096337	AK096337 Homo sapi
15		216	100.0	3862	6	AX026746	AX026746 Sequence
16		216	100.0	3862	9	AF279656	AF279656 Homo sapi
17		216	100.0	4250	9	AB037789	AB037789 Homo sapi
18		216	100.0	6060	6	BD160721	BD160721 Primer fo
19		216	100.0	6060	9	AK027867	AK027867 Homo sapi
20		216	100.0	131823	2	AC010497	AC010497 Homo sapi
21	c	216	100.0	134349	9	AC010296	AC010296 Homo sapi
22		216	100.0	154061	9	AC008524	AC008524 Homo sapi
23		216	100.0	179647	2	AC108124	AC108124 Homo sapi
24	c	216	100.0	188207	2	AC010233	AC010233 Homo sapi
25	c	212.8	98.5	56835	2	AC025369	AC025369 Homo sapi
26		195.2	90.4	3018	10	AF288666	AF288666 Mus muscu
27	c	193.6	89.6	170386	2	AC124181	AC124181 Mus muscu
28		193.6	89.6	184366	10	AC121783	AC121783 Mus muscu
29		193.6	89.6	237974	2	AC094771	AC094771 Rattus no
30	c	193.6	89.6	253924	2	AC126707	AC126707 Rattus no
31		193.6	89.6	258786	2	AC125773	AC125773 Rattus no
32		55	25.5	1853	6	BD157986	BD157986 Primer fo
33		55	25.5	1853	9	AK022747	AK022747 Homo sapi
34		55	25.5	2581	6	BD158055	BD158055 Primer fo
35		55	25.5	2581	9	AK022831	AK022831 Homo sapi
36		55	25.5	3196	6	AX685971	AX685971 Sequence
37		55	25.5	3205	6	AX685967	AX685967 Sequence
38		55	25.5	3364	6	AX685975	AX685975 Sequence
39		55	25.5	4234	6	AX492975	AX492975 Sequence
40		55	25.5	5886	9	AF389427	AF389427 Homo sapi
41		55	25.5	5924	9	AB040912	AB040912 Homo sapi
42		55	25.5	5925	9	AF389430	AF389430 Homo sapi
43		55	25.5	5943	9	AF389428	AF389428 Homo sapi
44		55	25.5	6111	9	AF389429	AF389429 Homo sapi
45		55	25.5	177657	9	AC018900	AC018900 Homo sapi

ALIGNMENTS

RESULT 1
AX026743
LOCUS AX026743 216 bp DNA linear PAT 16-SEP-2000
DEFINITION Sequence 3 from Patent WO0031252.
ACCESSION AX026743
VERSION AX026743.1 GI:10187888
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Klostermann,A. and Behl,C.
TITLE Human semaphorin 6a-1 (sema6a-a), a gene involved in neuronal
development and regeneration mechanisms during apoptosis, and its

```
          use as a potential drug target
  JOURNAL   Patent: WO 0031252-A 3 02-JUN-2000;
          KLOSTERMANN ANDREAS (DE) ; MAX PLANCK GESELLSCHAFT (DE) ; BEHL
          CHRISTIAN (DE)
FEATURES             Location/Qualifiers
     source          1. .216
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
     CDS             <1. .>216
                     /note="unnamed protein product"
                     /codon_start=1
                     /protein_id="CAC09108.1"
                     /db_xref="GI:10187889"
                     /translation="PPPAPQRVDSIQVHSSQPSGQAVTVSRQPSLNAYNSLTRSGLKR
                     TPSLKPDVPPKPSFAPLSTSMKPNDACT"
BASE COUNT       45 a     85 c     51 g     35 t
ORIGIN

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  Best Local Similarity   100.0%;  Pred. No. 1.1e-41;
  Matches  216;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CCGCCGCCCGCCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CCGCCGCCCGCCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC 60

Qy         61 CAGGCCGTGACTGTCTCGAGGCAGCCCAGCCTCAACGCCTACAACTCACTGACAAGGTCG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CAGGCCGTGACTGTCTCGAGGCAGCCCAGCCTCAACGCCTACAACTCACTGACAAGGTCG 120

Qy        121 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCC 180

Qy        181 CTTTCCACATCCATGAAGCCCAATGATGCGTGTACA 216
              ||||||||||||||||||||||||||||||||||||
Db        181 CTTTCCACATCCATGAAGCCCAATGATGCGTGTACA 216


RESULT 2
BD155987
LOCUS       BD155987                2123 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  Primer for synthesizing full-length cDNA and use thereof.
ACCESSION   BD155987
VERSION     BD155987.1  GI:27861745
KEYWORDS    JP 2002191363-A/10830.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 2123)
  AUTHORS   Ota,T., Isogai,T., Nishikawa,T., Hayashi,K., Saito,K., Yamamoto,J.,
            Ishii,S., Sugiyama,T., Wakamatsu,A., Nagai,K. and Otsuki,T.
  TITLE     Primer for synthesizing full-length cDNA and use thereof
  JOURNAL   Patent: JP 2002191363-A 10830 09-JUL-2002;
            HELIX RESEARCH INSTITUTE
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002191363-A/10830
            PD   09-JUL-2002
            PF   28-JUL-2000 JP 2000280990
            PI   TOSHIO OTA,TAKAO ISOGAI,TETSUO NISHIKAWA,KOJI HAYASHI,KAORU
            PI   SAITO,
            PI   JUNICHI YAMAMOTO,SHIZUKO ISHII,TOMOYASU SUGIYAMA,AI WAKAMATSU,
            PI   KEIICHI NAGAI,TETSUJI OTSUKI
            PC
            C12N15/09,C07K14/47,C07K16/18,C12N1/15,C12N1/19,C12N1/21,C12N5/ PC
             10,
            PC   C12P21/02,C12Q1/68//C12P21/08,G06F17/30,C12N15/00,C12N5/00 CC
             Primer for synthesizing full-length cDNA and use thereof FH   Key
                       Location/Qualifiers
            FT   CDS             (127). .(1647).
FEATURES             Location/Qualifiers
     source          1. .2123
                     /organism="Homo sapiens"
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BASE COUNT      550 a    664 c    528 g    381 t
ORIGIN

  Query Match             100.0%;  Score 216;  DB 6;  Length 2123;
  Best Local Similarity   100.0%;  Pred. No. 8.4e-42;
  Matches  216;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CCGCCGCCCGCCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC 60
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Db       1432 CCGCCGCCCGCCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC 1491

Qy         61 CAGGCCGTGACTGTCTCGAGGCAGCCCAGCCTCAACGCCTACAACTCACTGACAAGGTCG 120
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Db       1492 CAGGCCGTGACTGTCTCGAGGCAGCCCAGCCTCAACGCCTACAACTCACTGACAAGGTCG 1551

Qy        121 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1552 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCC 1611

Qy        181 CTTTCCACATCCATGAAGCCCAATGATGCGTGTACA 216
              ||||||||||||||||||||||||||||||||||||
Db       1612 CTTTCCACATCCATGAAGCCCAATGATGCGTGTACA 1647


RESULT 3
AK027439
LOCUS       AK027439                2123 bp    mRNA    linear   PRI 01-AUG-2002
DEFINITION  Homo sapiens cDNA FLJ14533 fis, clone NT2RM2000407, moderately
            similar to Mus musculus semaphorin VIa mRNA.
ACCESSION   AK027439
VERSION     AK027439.1  GI:14042113
KEYWORDS    oligo capping; fis (full insert sequence).
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Isogai,T., Ota,T., Hayashi,K., Sugiyama,T., Otsuki,T., Suzuki,Y.,
            Nishikawa,T., Nagai,K., Sugano,S., Shiratori,A., Sudo,H.,
            Wagatsuma,M., Hosoiri,T., Kaku,Y., Kodaira,H., Kondo,H.,
            Sugawara,M., Takahashi,M., Chiba,Y., Ishida,S., Murakawa,K.,
            Ono,Y., Takiguchi,S., Watanabe,S., Kimura,K., Murakami,K.,
            Ishii,S., Kawai,Y., Saito,K., Yamamoto,J., Wakamatsu,A.,
            Nakamura,Y., Nagahari,K., Masuho,Y., Ninomiya,K. and Iwayanagi,T.
  TITLE     NEDO human cDNA sequencing project
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 2123)
  AUTHORS   Isogai,T. and Otsuki,T.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-MAY-2001) Takao Isogai, Helix Research Institute,
            Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
            (E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)
COMMENT     NEDO human cDNA sequencing project supported by Ministry of
            Economy, Trade and Industry of Japan; cDNA full insert sequencing:
            Research Association for Biotechnology; cDNA library construction,
            5'- & 3'-end one pass sequencing and clone selection: Helix
            Research Institute (supported by Japan Key Technology Center etc.)
            and Department of Virology, Institute of Medical Science,
            University of Tokyo.
FEATURES             Location/Qualifiers
     source          1. .2123
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                     /db_xref="taxon:9606"
                     /clone="NT2RM2000407"
                     /cell_line="NT2"
                     /cell_type="teratocarcinoma"
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                neuronal precursor cells."
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                /protein_id="BAB55111.1"
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                GRCERHGKCKKTCIASRDPYCGWIKEGGACSHLSPNSRLTFEQDIERGNTDGLGDCHN
                SFVALNGVIRESYLKGHDQLVPVTLLAIAVILAFVMGAVFSGITVYCVCDHRRKDVAV
                VQRKEKELTHSRRGSMSSVTKLSGLFGDTQSKDPKPEAILTPLMHNGKLATPGNTAKM
                LIKADQHHLDLTALPTPESTPTLQQKRKPSRGSREWERNQNLINACTKDMPPMGSPVI
                PTDLPLRASPSHIPSVVVLPITQQGYQHEYVDQPKMSEVAQMALEDQAATLEYKTIKE
                HLSSKSPNHGVNLVENLDSLPPKVPQREASLGPPGASLSQTGLSKRLEMHHSSSYGVD
                YKRSYPTNSLTRSHQATTLKRNNTNSSNSSHLSRNQSFGRGDNPPPAPQRVDSIQVHS
                SQPSGQAVTVSRQPSLNAYNSLTRSGLKRTPSLKPDVPPKPSFAPLSTSMKPNDACT"
BASE COUNT      550 a    664 c    528 g    381 t
ORIGIN

  Query Match           100.0%;  Score 216;  DB 9;  Length 2123;
  Best Local Similarity  100.0%;  Pred. No. 8.4e-42;
  Matches  216;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CCGCCGCCCGCCCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1432 CCGCCGCCCGCCCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC 1491

Qy         61 CAGGCCGTGACTGTCTCGAGGCAGCCCAGCCTCAACGCCTACAACTCACTGACAAGGTCG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1492 CAGGCCGTGACTGTCTCGAGGCAGCCCAGCCTCAACGCCTACAACTCACTGACAAGGTCG 1551

Qy        121 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1552 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCC 1611

Qy        181 CTTTCCACATCCATGAAGCCCAATGATGCGTGTACA 216
              |||||||||||||||||||||||||||||||||||
Db       1612 CTTTCCACATCCATGAAGCCCAATGATGCGTGTACA 1647


RESULT 4
BD127394
LOCUS       BD127394                2227 bp    DNA     linear   PAT 18-SEP-2002
DEFINITION  Primer for synthesizing full-length cDNA and use thereof.
ACCESSION   BD127394
VERSION     BD127394.1  GI:23222339
KEYWORDS    JP 2002017375-A/2825.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 2227)
  AUTHORS   Ota,T., Nishikawa,T., Isogai,T., Hayashi,K., Ishii,S., Kawai,Y.,
            Wakamatsu,A., Sugiyama,T., Nagai,K., Kojima,S., Otsuki,T. and
            Koga,H.
  TITLE     Primer for synthesizing full-length cDNA and use thereof
  JOURNAL   Patent: JP 2002017375-A 2825 22-JAN-2002;
            HELIX RESEARCH INSTITUTE
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002017375-A/2825
            PD   22-JAN-2002
            PF   07-JUL-2000 JP 2000253172
            PI   TOSHIO OTA,TETSUO NISHIKAWA,TAKAO ISOGAI,KOJI HAYASHI,SHIZUKO
            PI   ISHII,
            PI   YURI KAWAI,AI WAKAMATSU,TOMOYASU SUGIYAMA,KEIICHI NAGAI, PI
            SHINICHI KOJIMA,
            PI   TETSUJI OTSUKI,HISASHI KOGA
            PC
            C12N15/09,C07K14/47,C07K16/18,C12N1/15,C12N1/19,C12N1/21,C12N5/ PC
             10,
            PC   C12P21/02,C12Q1/68//C12P21/08,G06F17/30,C12N15/00,C12N5/00 CC
             Primer for synthesizing full-length cDNA and use thereof FH   Key
                     Location/Qualifiers
            FT   CDS             (56). .(1741).

FEATURES             Location/Qualifiers
     source          1. .2227
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT      567 a    700 c    560 g    400 t
ORIGIN

  Query Match           100.0%;  Score 216;  DB 6;  Length 2227;
  Best Local Similarity  100.0%;  Pred. No. 8.4e-42;
  Matches  216;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CCGCCGCCCGCCCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1526 CCGCCGCCCGCCCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC 1585

Qy         61 CAGGCCGTGACTGTCTCGAGGCAGCCCAGCCTCAACGCCTACAACTCACTGACAAGGTCG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1586 CAGGCCGTGACTGTCTCGAGGCAGCCCAGCCTCAACGCCTACAACTCACTGACAAGGTCG 1645

Qy        121 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1646 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCC 1705

Qy        181 CTTTCCACATCCATGAAGCCCAATGATGCGTGTACA 216
              |||||||||||||||||||||||||||||||||||
Db       1706 CTTTCCACATCCATGAAGCCCAATGATGCGTGTACA 1741


RESULT 5
AK074975
LOCUS       AK074975                2227 bp    mRNA    linear   PRI 03-SEP-2002
DEFINITION  Homo sapiens cDNA FLJ90494 fis, clone NT2RP3003614.
ACCESSION   AK074975
VERSION     AK074975.1  GI:22760768
KEYWORDS    oligo capping; fis (full insert sequence).
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Isogai,T., Ota,T., Nishikawa,T., Hayashi,K., Otsuki,T.,
            Sugiyama,T., Suzuki,Y., Nagai,K., Sugano,S., Ishii,S.,
            Kawai-Hio,Y., Saito,K., Yamamoto,J., Wakamatsu,A., Nakamura,Y.,
            Kojima,S., Nagahari,K., Masuho,Y., Ono,T., Okano,K., Yoshikawa,Y.,
            Aotsuka,S., Sasaki,N., Hattori,A., Okumura,K., Iwayanagi,T. and
            Ninomiya,K.
  TITLE     NEDO human cDNA sequencing project
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 2227)
  AUTHORS   Isogai,T. and Otsuki,T.
  TITLE     Direct Submission
  JOURNAL   Submitted (25-MAR-2002) Takao Isogai, Helix Research Institute,
            Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
            (E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)
COMMENT     NEDO human cDNA sequencing project supported by Ministry of
            Economy, Trade and Industry of Japan; cDNA full insert sequencing:
            Research Association for Biotechnology; cDNA library construction:
            Institute of Medical Science, University of Tokyo, Laboratory of
            Genome Structure, Human Genome Center; cDNA 5'- & 3'-end one pass
            sequencing and clone selection: Helix Research Institute (supported
            by Japan Key Technology Center etc.).
FEATURES             Location/Qualifiers
     source          1. .2227
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="NT2RP3003614"
                     /cell_line="NT2"
                     /cell_type="teratocarcinoma"
                     /clone_lib="NT2RP3"
                     /note="cloning vector: pME18SFL3-mRNA from NT2 neuronal
                     precursor cells after 2-weeks retinoic acid (RA)
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                SFVALNGHSSSLLPSTTTSDSTAQEGYESRGGMLDWKHLLDSPDSTDPLGAVSSHNHQ
                DKKGVIRESYLKGHDQLVPVTLLAIAVILAFVMGAVFSGITVYCVCDHRRKDVAVVQR
                KEKELTHSRRGSMSSVTKLSGLFGDTQSKDPKPEAILTPLMHNGKLATPGNTAKMLIK
                ADQHHLDLTALPTPESTPTLQQKRKPSRGSREWERNQNLINACTKDMPPMGSPVIPTD
                LPLRASPSHIPSVVVLPITQQGYQHEYVDQPKMSEVAQMALEDQAATLEYKTIKEHLS
                SKSPNHGVNLVENLDSLPPKVPQREASLGPPGASLSQTGLSKRLEMHHSSSYGVDYKR
                SYPTNSLTRSHQATTLKRNNTNSSNSSHLSRNQSFGRGDSPPPAPQRVDSIQVHSSQP
                SGQAVTVSRQPSLNAYNSLTRSGLKRTPSLKPDVPPKPSFAPLSTSMKPNDACT"
BASE COUNT      567 a    700 c    560 g    400 t
ORIGIN

  Query Match           100.0%;  Score 216;  DB 9;  Length 2227;
  Best Local Similarity  100.0%;  Pred. No. 8.4e-42;
  Matches  216;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CCGCCGCCCGCCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1526 CCGCCGCCCGCCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC 1585

Qy         61 CAGGCCGTGACTGTCTCGAGGCAGCCCAGCCTCAACGCCTACAACTCACTGACAAGGTCG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1586 CAGGCCGTGACTGTCTCGAGGCAGCCCAGCCTCAACGCCTACAACTCACTGACAAGGTCG 1645

Qy        121 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1646 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCC 1705

Qy        181 CTTTCCACATCCATGAAGCCCAATGATGCGTGTACA 216
              |||||||||||||||||||||||||||||||||||
Db       1706 CTTTCCACATCCATGAAGCCCAATGATGCGTGTACA 1741


RESULT 6
BD157826
LOCUS       BD157826                2293 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  Primer for synthesizing full-length cDNA and use thereof.
ACCESSION   BD157826
VERSION     BD157826.1  GI:27863584
KEYWORDS    JP 2002191363-A/12669.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 2293)
  AUTHORS   Ota,T., Isogai,T., Nishikawa,T., Hayashi,K., Saito,K., Yamamoto,J.,
            Ishii,S., Sugiyama,T., Wakamatsu,A., Nagai,K. and Otsuki,T.
  TITLE     Primer for synthesizing full-length cDNA and use thereof
  JOURNAL   Patent: JP 2002191363-A 12669 09-JUL-2002;
            HELIX RESEARCH INSTITUTE
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002191363-A/12669
            PD   09-JUL-2002
            PF   28-JUL-2000 JP 2000280990
            PI   TOSHIO OTA,TAKAO ISOGAI,TETSUO NISHIKAWA,KOJI HAYASHI,KAORU
            PI   SAITO,
            PI   JUNICHI YAMAMOTO,SHIZUKO ISHII,TOMOYASU SUGIYAMA,AI WAKAMATSU,
            PI   KEIICHI NAGAI,TETSUJI OTSUKI
            PC
            C12N15/09,C07K14/47,C07K16/18,C12N1/15,C12N1/19,C12N1/21,C12N5/ PC
             10,
            PC   C12P21/02,C12Q1/68//C12P21/08,G06F17/30,C12N15/00,C12N5/00 CC
             Primer for synthesizing full-length cDNA and use thereof FH   Key
                      Location/Qualifiers
            FT   CDS             (138). .(1823).
FEATURES             Location/Qualifiers
     source          1. .2293
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT      579 a    713 c    581 g    420 t
ORIGIN

  Query Match           100.0%;  Score 216;  DB 6;  Length 2293;
  Best Local Similarity  100.0%;  Pred. No. 8.4e-42;
  Matches  216;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CCGCCGCCCGCCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1608 CCGCCGCCCGCCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC 1667

Qy         61 CAGGCCGTGACTGTCTCGAGGCAGCCCAGCCTCAACGCCTACAACTCACTGACAAGGTCG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1668 CAGGCCGTGACTGTCTCGAGGCAGCCCAGCCTCAACGCCTACAACTCACTGACAAGGTCG 1727

Qy        121 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1728 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCC 1787

Qy        181 CTTTCCACATCCATGAAGCCCAATGATGCGTGTACA 216
              |||||||||||||||||||||||||||||||||||
Db       1788 CTTTCCACATCCATGAAGCCCAATGATGCGTGTACA 1823


RESULT 7
AK027471
LOCUS       AK027471                2293 bp    mRNA    linear   PRI 01-AUG-2002
DEFINITION  Homo sapiens cDNA FLJ14565 fis, clone NT2RM4000233, highly similar
            to Mus musculus semaphorin VIa mRNA.
ACCESSION   AK027471
VERSION     AK027471.1  GI:14042170
KEYWORDS    oligo capping; fis (full insert sequence).
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Isogai,T., Ota,T., Hayashi,K., Sugiyama,T., Otsuki,T., Suzuki,Y.,
            Nishikawa,T., Nagai,K., Sugano,S., Shiratori,A., Sudo,H.,
            Wagatsuma,M., Hosoiri,T., Kaku,Y., Kodaira,H., Kondo,H.,
            Sugawara,M., Takahashi,M., Chiba,Y., Ishida,S., Murakawa,K.,
            Ono,Y., Takiguchi,S., Watanabe,S., Kimura,K., Murakami,K.,
            Ishii,S., Kawai,Y., Saito,K., Yamamoto,J., Wakamatsu,A.,
            Nakamura,Y., Nagahari,K., Masuho,Y., Ninomiya,K. and Iwayanagi,T.
  TITLE     NEDO human cDNA sequencing project
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 2293)
  AUTHORS   Isogai,T. and Otsuki,T.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-MAY-2001) Takao Isogai, Helix Research Institute,
            Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
            (E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)
COMMENT     NEDO human cDNA sequencing project supported by Ministry of
            Economy, Trade and Industry of Japan; cDNA full insert sequencing:
            Research Association for Biotechnology; cDNA library construction,
            5'- & 3'-end one pass sequencing and clone selection: Helix
            Research Institute (supported by Japan Key Technology Center etc.)
            and Department of Virology, Institute of Medical Science,
            University of Tokyo.
FEATURES             Location/Qualifiers
     source          1. .2293
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="NT2RM4000233"
                     /cell_line="NT2"
                     /cell_type="teratocarcinoma"
                     /clone_lib="NT2RM4"
                     /note="cloning vector: pUC19FL3-mRNA from uninduced NT2
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                     neuronal precursor cells."
     CDS             138. .1826
                     /note="unnamed protein product"
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                     /db_xref="GI:14042171"
                     /translation="MSVYNSEKCSYDGVEDKRIMGMQLDRASSSLYVAFSTCVIKVPL
                     GRCERHGKCKKTCIASRDPYCGWIKEGGACSHLSPNSRLTFEQDIERGNTDGLGDCHN
                     SFVALNGHSSSLLPSTTTSDSTAQEGYESRGGMLDWKHLLDSPDSTDPLGAVSSHNHQ
                     DKKGVIRESYLKGHDQLVPVTLLAIAVILAFVMGAVFSGITVYCVCDHRRKDVAVVQR
                     KEKELTHSRRGSMSSVTKLSGLFGDTQSKDPKPEAILTPLMHNGKLATPGNTAKMLIK
                     ADQHHLDLTALPTPESTPTLQQKRKPSRGSREWERNQNLINACTKDMPPMGSPVIPTD
                     LPLRASPSHIPSVVVLPITQQGYQHEYVDQPKMSEVAQMALEDQAATLEYKTIKEHLS
                     SKSPNHGVNLVENLDSLPPKVPQREASLGPPGASLSQTGLSKRLEMHHSSSYGVDYKR
                     SYPTNSLTRSHQATTLKRNNTNSSNSSHLSRNQSFGRGDNPPPAPQRVDSIQVHSSQP
                     SGQAVTVSRQPSLNAYNSLTRSGLKRTPSLKPDVPPKPSFAPLSTSMKPNDACT"
BASE COUNT      579 a    713 c    581 g    420 t
ORIGIN

  Query Match             100.0%;  Score 216;  DB 9;  Length 2293;
  Best Local Similarity   100.0%;  Pred. No. 8.4e-42;
  Matches  216;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CCGCCGCCCGCCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1608 CCGCCGCCCGCCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC 1667

Qy         61 CAGGCCGTGACTGTCTCGAGGCAGCCCAGCCTCAACGCCTACAACTCACTGACAAGGTCG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1668 CAGGCCGTGACTGTCTCGAGGCAGCCCAGCCTCAACGCCTACAACTCACTGACAAGGTCG 1727

Qy        121 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1728 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCC 1787

Qy        181 CTTTCCACATCCATGAAGCCCAATGATGCGTGTACA 216
              |||||||||||||||||||||||||||||||||||
Db       1788 CTTTCCACATCCATGAAGCCCAATGATGCGTGTACA 1823


RESULT 8
BD159853
LOCUS       BD159853               2306 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  Primer for synthesizing full-length cDNA and use thereof.
ACCESSION   BD159853
VERSION     BD159853.1  GI:27865611
KEYWORDS    JP 2002191363-A/14696.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 2306)
  AUTHORS   Ota,T., Isogai,T., Nishikawa,T., Hayashi,K., Saito,K., Yamamoto,J.,
            Ishii,S., Sugiyama,T., Wakamatsu,A., Nagai,K. and Otsuki,T.
  TITLE     Primer for synthesizing full-length cDNA and use thereof
  JOURNAL   Patent: JP 2002191363-A 14696 09-JUL-2002;
            HELIX RESEARCH INSTITUTE
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002191363-A/14696
            PD   09-JUL-2002
            PF   28-JUL-2000 JP 2000280990
            PI   TOSHIO OTA,TAKAO ISOGAI,TETSUO NISHIKAWA,KOJI HAYASHI,KAORU
            PI   SAITO,
            PI   JUNICHI YAMAMOTO,SHIZUKO ISHII,TOMOYASU SUGIYAMA,AI WAKAMATSU,
            PI   KEIICHI NAGAI,TETSUJI OTSUKI
            PC
            C12N15/09,C07K14/47,C07K16/18,C12N1/15,C12N1/19,C12N1/21,C12N5/ PC
             10,
            PC   C12P21/02,C12Q1/68//C12P21/08,G06F17/30,C12N15/00,C12N5/00 CC
             Primer for synthesizing full-length cDNA and use thereof FH   Key
                      Location/Qualifiers
            FT   CDS             (109). .(1830).
FEATURES              Location/Qualifiers
     source           1. .2306
                      /organism="Homo sapiens"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:9606"
BASE COUNT      579 a    739 c    577 g    411 t
ORIGIN

  Query Match             100.0%;  Score 216;  DB 6;  Length 2306;
  Best Local Similarity   100.0%;  Pred. No. 8.3e-42;
  Matches  216;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CCGCCGCCCGCCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1615 CCGCCGCCCGCCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC 1674

Qy         61 CAGGCCGTGACTGTCTCGAGGCAGCCCAGCCTCAACGCCTACAACTCACTGACAAGGTCG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1675 CAGGCCGTGACTGTCTCGAGGCAGCCCAGCCTCAACGCCTACAACTCACTGACAAGGTCG 1734

Qy        121 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1735 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCC 1794

Qy        181 CTTTCCACATCCATGAAGCCCAATGATGCGTGTACA 216
              |||||||||||||||||||||||||||||||||||
Db       1795 CTTTCCACATCCATGAAGCCCAATGATGCGTGTACA 1830


RESULT 9
AK027654
LOCUS       AK027654               2306 bp    mRNA    linear   PRI 01-AUG-2002
DEFINITION  Homo sapiens cDNA FLJ14748 fis, clone NT2RP3002869, highly similar
            to Mus musculus semaphorin VIa mRNA.
ACCESSION   AK027654
VERSION     AK027654.1  GI:14042491
KEYWORDS    oligo capping; fis (full insert sequence).
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Isogai,T., Ota,T., Hayashi,K., Sugiyama,T., Otsuki,T., Suzuki,Y.,
            Nishikawa,T., Nagai,K., Sugano,S., Shiratori,A., Sudo,H.,
            Wagatsuma,M., Hosoiri,T., Kaku,Y., Kodaira,H., Kondo,H.,
            Sugawara,M., Takahashi,M., Chiba,Y., Ishida,S., Murakawa,K.,
            Ono,Y., Takiguchi,S., Watanabe,S., Kimura,K., Murakami,K.,
            Ishii,S., Kawai,Y., Saito,K., Yamamoto,J., Wakamatsu,A.,
            Nakamura,Y., Nagahari,K., Masuho,Y., Ninomiya,K. and Iwayanagi,T.
  TITLE     NEDO human cDNA sequencing project
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 2306)
  AUTHORS   Isogai,T. and Otsuki,T.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-MAY-2001) Takao Isogai, Helix Research Institute,
            Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
            (E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)
COMMENT     NEDO human cDNA sequencing project supported by Ministry of
            Economy, Trade and Industry of Japan; cDNA full insert sequencing:
            Research Association for Biotechnology; cDNA library construction,
            5'- & 3'-end one pass sequencing and clone selection: Helix
            Research Institute (supported by Japan Key Technology Center etc.)
            and Department of Virology, Institute of Medical Science,
            University of Tokyo.
FEATURES              Location/Qualifiers
     source           1. .2306
                      /organism="Homo sapiens"
                      /mol_type="mRNA"
                      /db_xref="taxon:9606"
                      /clone="NT2RP3002869"
                      /cell_line="NT2"
                      /cell_type="teratocarcinoma"
                      /clone_lib="NT2RP3"
                      /note="cloning vector: pME18SFL3-mRNA from NT2 neuronal
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                precursor cells after 2-weeks retinoic acid (RA)
                induction."
     CDS        109. .1833
                /note="unnamed protein product"
                /codon_start=1
                /protein_id="BAB55269.1"
                /db_xref="GI:14042492"
                /translation="MDEAVPSIFNRPWFLRTMVRCSYDGVEDKRIMGMQLDRASSSLY
                VAFSTCVIKVPLGRCERHGKCKKTCIASRDPYCGWIKEGGACSHLSPNSRLTFEQDIE
                RGNTDGLGDCHNSFVALNGHSSSLLPSTTTSDSTAQEGYESRGGMLDWKHLLDSPDST
                DPLGAVSSHNHQDKKGVIRESYLKGHDQLVPVTLLAIAVILAFVMGAVFSGITVYCVC
                DHRRKDVAVVQRKEKELTHSRRGSMSSVTKLSGLFGDTQSKDPKPEAILTPLMHNGKL
                ATPGNTAKMLIKADQHHLDLTALPTPESTPTLQQKRKPSRGSREWERNQNLINACTKD
                MPPMGSPVIPTDLPLRASPSHIPSVVVLPITQQGYQHEYVDQPKMSEVAQMALEDQAA
                TLEYKTIKEHLSSKSPNHGVNLVENLDSLPPKVPQREASLGPPGASLSQTGLSKRLEM
                HHSSSYGVDYKRSYPTNSLTRSHQATTLKRNNTNSSNSSHLSRNQSFGRGDNPPPAPQ
                RVDSIQVHSSQPSGQAVTVSRQPSLNAYNSLTRSGLKRTPSLKPDVPPKPSFAPLSTS
                MKPNDACT"
BASE COUNT      579 a    739 c    577 g    411 t
ORIGIN

  Query Match             100.0%;  Score 216;  DB 9;  Length 2306;
  Best Local Similarity   100.0%;  Pred. No. 8.3e-42;
  Matches  216;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CCGCCGCCCGCCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1615 CCGCCGCCCGCCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC 1674

Qy         61 CAGGCCGTGACTGTCTCGAGGCAGCCCAGCCTCAACGCCTACAACTCACTGACAAGGTCG 120
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Db       1675 CAGGCCGTGACTGTCTCGAGGCAGCCCAGCCTCAACGCCTACAACTCACTGACAAGGTCG 1734

Qy        121 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCC 180
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Db       1735 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCC 1794

Qy        181 CTTTCCACATCCATGAAGCCCAATGATGCGTGTACA 216
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Db       1795 CTTTCCACATCCATGAAGCCCAATGATGCGTGTACA 1830


RESULT 10
BD159617
LOCUS       BD159617                3041 bp    DNA     linear   PAT 17-JAN-2003
DEFINITION  Primer for synthesizing full-length cDNA and use thereof.
ACCESSION   BD159617
VERSION     BD159617.1  GI:27865375
KEYWORDS    JP 2002191363-A/14460.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 3041)
  AUTHORS   Ota,T., Isogai,T., Nishikawa,T., Hayashi,K., Saito,K., Yamamoto,J.,
            Ishii,S., Sugiyama,T., Wakamatsu,A., Nagai,K. and Otsuki,T.
  TITLE     Primer for synthesizing full-length cDNA and use thereof
  JOURNAL   Patent: JP 2002191363-A 14460 09-JUL-2002;
            HELIX RESEARCH INSTITUTE
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002191363-A/14460
            PD   09-JUL-2002
            PF   28-JUL-2000 JP 2000280990
            PI   TOSHIO OTA,TAKAO ISOGAI,TETSUO NISHIKAWA,KOJI HAYASHI,KAORU
            PI   SAITO,
            PI   JUNICHI YAMAMOTO,SHIZUKO ISHII,TOMOYASU SUGIYAMA,AI WAKAMATSU,
            PI   KEIICHI NAGAI,TETSUJI OTSUKI
            PC
            C12N15/09,C07K14/47,C07K16/18,C12N1/15,C12N1/19,C12N1/21,C12N5/ PC
             10,
            PC   C12P21/02,C12Q1/68//C12P21/08,G06F17/30,C12N15/00,C12N5/00 CC
             Primer for synthesizing full-length cDNA and use thereof FH   Key
                     Location/Qualifiers
          FT   CDS             (85). .(2181).
FEATURES             Location/Qualifiers
     source          1. .3041
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT      804 a    886 c    714 g    637 t
ORIGIN

  Query Match             100.0%;  Score 216;  DB 6;  Length 3041;
  Best Local Similarity   100.0%;  Pred. No. 8e-42;
  Matches  216;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CCGCCGCCCGCCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC 60
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Db       1966 CCGCCGCCCGCCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC 2025

Qy         61 CAGGCCGTGACTGTCTCGAGGCAGCCCAGCCTCAACGCCTACAACTCACTGACAAGGTCG 120
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Db       2026 CAGGCCGTGACTGTCTCGAGGCAGCCCAGCCTCAACGCCTACAACTCACTGACAAGGTCG 2085

Qy        121 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCC 180
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Db       2086 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCC 2145

Qy        181 CTTTCCACATCCATGAAGCCCAATGATGCGTGTACA 216
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Db       2146 CTTTCCACATCCATGAAGCCCAATGATGCGTGTACA 2181


RESULT 11
AK027501
LOCUS       AK027501                3041 bp    mRNA    linear   PRI 01-AUG-2002
DEFINITION  Homo sapiens cDNA FLJ14595 fis, clone NT2RM4002194, highly similar
            to Mus musculus semaphorin VIa mRNA.
ACCESSION   AK027501
VERSION     AK027501.1  GI:14042222
KEYWORDS    oligo capping; fis (full insert sequence).
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Isogai,T., Ota,T., Hayashi,K., Sugiyama,T., Otsuki,T., Suzuki,Y.,
            Nishikawa,T., Nagai,K., Sugano,S., Shiratori,A., Sudo,H.,
            Wagatsuma,M., Hosoiri,T., Kaku,Y., Kodaira,H., Kondo,H.,
            Sugawara,M., Takahashi,M., Chiba,Y., Ishida,S., Murakawa,K.,
            Ono,Y., Takiguchi,S., Watanabe,S., Kimura,K., Murakami,K.,
            Ishii,S., Kawai,Y., Saito,K., Yamamoto,J., Wakamatsu,A.,
            Nakamura,Y., Nagahari,K., Masuho,Y., Ninomiya,K. and Iwayanagi,T.
  TITLE     NEDO human cDNA sequencing project
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 3041)
  AUTHORS   Isogai,T. and Otsuki,T.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-MAY-2001) Takao Isogai, Helix Research Institute,
            Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
            (E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)
COMMENT     NEDO human cDNA sequencing project supported by Ministry of
            Economy, Trade and Industry of Japan; cDNA full insert sequencing:
            Research Association for Biotechnology; cDNA library construction,
            5'- & 3'-end one pass sequencing and clone selection: Helix
            Research Institute (supported by Japan Key Technology Center etc.)
            and Department of Virology, Institute of Medical Science,
            University of Tokyo.
FEATURES             Location/Qualifiers
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                     /clone_lib="NT2RM4"
                     /note="cloning vector: pUC19FL3-mRNA from uninduced NT2
                     neuronal precursor cells."
     CDS             85. .2184
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                     /db_xref="GI:14042223"
                     /translation="MLDIASVFTGRFKEQKSPDSTWTPVPDERVPKPRPGCCAGSSSL
                     ERYATSNEFPDDTLNFIKTHPLMDEAVPSIFNRPWFLRTMVRYRLTKIAVDTAAGPYQ
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                     LDRASSSLYVAFSTCVIKVPLGRCERHGKCKKTCIASRDPYCGWIKEGGACSHLSPNS
                     RLTFEQDIERGNTDGLGDCHNSFVALNGHSSSLLPSTTTSDSTAQEGYESRGGMLDWK
                     HLLDSPDSTDPLGAVSSHNHQDKKGVIRESYLKGHDQLVPVTLLAIAVILAFVMGAVF
                     SGITVYCVCDHRRKDVAVVQRKEKELTHSRRGSMSSVTKLSGLFGDTQSKDPKPEAIL
                     TPLMHNGKLATPGNTAKMLIKADQHHLDLTALPTPESTPTLQQKRKPSRGSREWERNQ
                     NLINACTKDMPPMGSPVIPTDLPLRASPSHIPSVVVLPITQQGYQHEYVDQPKMSEVA
                     QMALEDQAATLEYKTIKEHLSSKSPNHGVNLVENLDSLPPKVPQREASLGPPGASLSQ
                     TGLSKRLEMHHSSSYGVDYKRSYPTNSLTRSHQATTLKRNNTNSSNSSHLSRNQSFGR
                     GDNPPPAPQRVDSIQVHSSQPSGQAVTVSRQPSLNAYNSLTRSGLKRTPSLKPDVPPK
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BASE COUNT      804 a    886 c    714 g    637 t
ORIGIN

  Query Match           100.0%;  Score 216;  DB 9;  Length 3041;
  Best Local Similarity  100.0%;  Pred. No. 8e-42;
  Matches  216;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CCGCCGCCCGCCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1966 CCGCCGCCCGCCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC 2025

Qy         61 CAGGCCGTGACTGTCTCGAGGCAGCCCAGCCTCAACGCCTACAACTCACTGACAAGGTCG 120
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Db       2026 CAGGCCGTGACTGTCTCGAGGCAGCCCAGCCTCAACGCCTACAACTCACTGACAAGGTCG 2085

Qy        121 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2086 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCC 2145

Qy        181 CTTTCCACATCCATGAAGCCCAATGATGCGTGTACA 216
              |||||||||||||||||||||||||||||||||||
Db       2146 CTTTCCACATCCATGAAGCCCAATGATGCGTGTACA 2181


RESULT 12
AX026741
LOCUS       AX026741               3093 bp    DNA     linear   PAT 16-SEP-2000
DEFINITION  Sequence 1 from Patent WO0031252.
ACCESSION   AX026741
VERSION     AX026741.1  GI:10187886
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Klostermann,A. and Behl,C.
  TITLE     Human semaphorin 6a-1 (sema6a-a), a gene involved in neuronal
            development and regeneration mechanisms during apoptosis, and its
            use as a potential drug target
  JOURNAL   Patent: WO 0031252-A 1 02-JUN-2000;
            KLOSTERMANN ANDREAS (DE) ; MAX PLANCK GESELLSCHAFT (DE) ; BEHL
            CHRISTIAN (DE)
FEATURES             Location/Qualifiers
     source          1. .3093
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
     CDS             1. .3093
                     /note="unnamed protein product"
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                     /db_xref="GI:10187887"
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                     IASVFTGRFKEQKSPDSTWTPVPDERVPKPRPGCCAGSSSLERYATSNEFPDDTLNFI
                     KTHPLMDEAVPSIFNRPWFLRTMVRYRLTKIAVDTAAGPYQNHTVVFLGSEKGIILKF
                     LARIGNSGFLNDSLFLEEMSVYNSEKCSYDGVEDKRIMGMQLDRASSSLYVAFSTCVI
                     KVPLGRCERHGKCKKTCIASRDPYCGWIKEGGACSHLSPNSRLTFEQDIERGNTDGLG
                     DCHNSFVALNGHSSSLLPSTTTSDSTAQEGYESRGGMLDWKHLLDSPDSTDPLGAVSS
                     HNHQDKKGVIRESYLKGHDQLVPVTLLAIAVILAFVMGAVFSGITVYCVCDHRRKDVA
                     VVQRKEKELTHSRRGSMSSVTKLSGLFGDTQSKDPKPEAILTPLMHNGKLATPGNTAK
                     MLIKADQHHLDLTALPTPESTPTLQQKRKPSRGSREWERNQNLINACTKDMPPMGSPV
                     IPTDLPLRASPSHIPSVVVLPITQQGYQHEYVDQPKMSEVAQMALEDQAATLEYKTIK
                     EHLSSKSPNHGVNLVENLDSLPPKVPQREASLGPPGASLSQTGLSKRLEMHHSSSYGV
                     DYKRSYPTNSLTRSHQATTLKRNNTNSSNSSHLSRNQSFGRGDNPPPAPQRVDSIQVH
                     SSQPSGQAVTVSRQPSLNAYNSLTRSGLKRTPSLKPDVPPKPSFAPLSTSMKPNDACT
                     "
BASE COUNT      813 a    855 c    765 g    660 t
ORIGIN

  Query Match           100.0%;  Score 216;  DB 6;  Length 3093;
  Best Local Similarity  100.0%;  Pred. No. 8e-42;
  Matches  216;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CCGCCGCCCGCCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC 60
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Db       2875 CCGCCGCCCGCCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC 2934

Qy         61 CAGGCCGTGACTGTCTCGAGGCAGCCCAGCCTCAACGCCTACAACTCACTGACAAGGTCG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2935 CAGGCCGTGACTGTCTCGAGGCAGCCCAGCCTCAACGCCTACAACTCACTGACAAGGTCG 2994

Qy        121 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCC 180
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Db       2995 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCC 3054

Qy        181 CTTTCCACATCCATGAAGCCCAATGATGCGTGTACA 216
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Db       3055 CTTTCCACATCCATGAAGCCCAATGATGCGTGTACA 3090


RESULT 13
AX099520
LOCUS       AX099520               3550 bp    DNA     linear   PAT 02-APR-2001
DEFINITION  Sequence 160 from Patent WO0119988.
ACCESSION   AX099520
VERSION     AX099520.1  GI:13538594
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Jacobs,K., Mccoy,J.M., Lavallie,E.R., Collins-Racie,L.A., Evans,C.,
            Merberg,D., Treacy,M., Bowman,M.R., Spaulding,V. and Agostino,M.J.
  TITLE     Secreted proteins and polynucleotides encoding them
  JOURNAL   Patent: WO 0119988-A 160 22-MAR-2001;
            Genetics Institute, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .3550
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
BASE COUNT      957 a    994 c    856 g    742 t      1 others
ORIGIN

  Query Match           100.0%;  Score 216;  DB 6;  Length 3550;
  Best Local Similarity  100.0%;  Pred. No. 7.9e-42;
  Matches  216;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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Qy          1 CCGCCGCCCGCCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC 60
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Db       2835 CCGCCGCCCGCCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC 2894

Qy         61 CAGGCCGTGACTGTCTCGAGGCAGCCCAGCCTCAACGCCTACAACTCACTGACAAGGTCG 120
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Db       2895 CAGGCCGTGACTGTCTCGAGGCAGCCCAGCCTCAACGCCTACAACTCACTGACAAGGTCG 2954

Qy        121 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCC 180
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Qy        181 CTTTCCACATCCATGAAGCCCAATGATGCGTGTACA 216
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Db       3015 CTTTCCACATCCATGAAGCCCAATGATGCGTGTACA 3050
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RESULT 14
AK096337
LOCUS       AK096337               3634 bp    mRNA    linear   PRI 15-JUL-2002
DEFINITION  Homo sapiens cDNA FLJ39018 fis, clone NT2RP7002594, highly similar
            to Homo sapiens semaphorin SEMA6A1 mRNA.
ACCESSION   AK096337
VERSION     AK096337.1  GI:21755807
KEYWORDS    oligo capping; fis (full insert sequence).
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Ninomiya,K., Wagatsuma,M., Kanda,K., Kondo,H., Yokoi,T.,
            Kodaira,H., Furuya,T., Takahashi,M., Kikkawa,E., Omura,Y., Abe,K.,
            Kamihara,K., Katsuta,N., Sato,K., Tanikawa,M., Yamazaki,M.,
            Sugiyama,T., Irie,R., Otsuki,T., Sato,H., Wakamatsu,A., Ishii,S.,
            Yamamoto,J., Isono,Y., Kawai-Hio,Y., Saito,K., Nishikawa,T.,
            Kimura,K., Yamashita,H., Matsuo,K., Nakamura,Y., Sekine,M.,
            Kikuchi,H., Murakawa,K., Kanehori,K., Takahashi-Fujii,A.,
            Oshima,A., Sugiyama,A., Kawakami,B., Suzuki,Y., Sugano,S.,
            Nagahari,K., Masuho,Y., Nagai,K. and Isogai,T.
  TITLE     NEDO human cDNA sequencing project
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 3634)
  AUTHORS   Isogai,T. and Yamamoto,J.
  TITLE     Direct Submission
  JOURNAL   Submitted (04-JUL-2002) Takao Isogai, PLJ Project(HRI Team); 2-6-7
            Kazusa-Kamatari, Kisarazu, Chiba 292-0812, Japan
            (E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)
COMMENT     NEDO human cDNA sequencing project supported by Ministry of
            Economy, Trade and Industry of Japan; cDNA full insert sequencing:
            Research Association for Biotechnology (RAB); cDNA library
            construction: Helix Research Institute (HRI) (supported by Japan
            Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB,
            HRI, and Biotechnology Center, National Institute of Technology and
            Evaluation; clone selection for full insert sequencing: HRI and
            RAB; annotation: HRI and RAB.
FEATURES             Location/Qualifiers
     source          1. .3634
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="NT2RP7002594"
                     /cell_line="NT2"
                     /cell_type="teratocarcinoma"
                     /clone_lib="NT2RP7"
                     /note="cloning vector: pME18SFL3-mRNA from NT2 neuronal
                     precursor cells after 5-weeks retinoic acid (RA)
                     induction."
BASE COUNT      990 a   1014 c    805 g    825 t
ORIGIN

  Query Match           100.0%;  Score 216;  DB 9;  Length 3634;
  Best Local Similarity  100.0%;  Pred. No. 7.9e-42;
  Matches  216;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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Qy          1 CCGCCGCCCGCCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC 60
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Qy         61 CAGGCCGTGACTGTCTCGAGGCAGCCCAGCCTCAACGCCTACAACTCACTGACAAGGTCG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3003 CAGGCCGTGACTGTCTCGAGGCAGCCCAGCCTCAACGCCTACAACTCACTGACAAGGTCG 3062

Qy        121 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCC 180
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Db       3063 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCC 3122

Qy        181 CTTTCCACATCCATGAAGCCCAATGATGCGTGTACA 216
              ||||||||||||||||||||||||||||||||||||
Db       3123 CTTTCCACATCCATGAAGCCCAATGATGCGTGTACA 3158
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RESULT 15
AX026746
LOCUS       AX026746               3862 bp    DNA     linear   PAT 16-SEP-2000
DEFINITION  Sequence 6 from Patent WO0031252.
ACCESSION   AX026746
VERSION     AX026746.1  GI:10187890
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Klostermann,A. and Behl,C.
  TITLE     Human semaphorin 6a-1 (sema6a-a), a gene involved in neuronal
            development and regeneration mechanisms during apoptosis, and its
            use as a potential drug target
  JOURNAL   Patent: WO 0031252-A 6 02-JUN-2000;
            KLOSTERMANN ANDREAS (DE) ; MAX PLANCK GESELLSCHAFT (DE) ; BEHL
            CHRISTIAN (DE)
FEATURES             Location/Qualifiers
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                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
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                     LKARLNCSVPGDSHFYFNILQAVTDVIRINGRDVVLATFSTPYNSIPGSAVCAYDMLD
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                     KTHPLMDEAVPSIFNRPWFLRTMVRYRLTKIAVDTAAGPYQNHTVVFLGSEKGIILKF
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                     DCHNSFVALNGHSSSLLPSTTTSDSTAQEGYESRGGMLDWKHLLDSPDSTDPLGAVSS
                     HNHQDKKGVIRESYLKGHDQLVPVTLLAIAVILAFVMGAVFSGITVYCVCDHRRKDVA
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                     MLIKADQHHLDLTALPTPESTPTLQQKRKPSRGSREWERNQNLINACTKDMPPMGSPV
                     IPTDLPLRASPSHIPSVVVLPITQQGYQHEYVDQPKMSEVAQMALEDQAATLEYKTIK
                     EHLSSKSPNHGVNLVENLDSLPPKVPQREASLGPPGASLSQTGLSKRLEMHHSSSYGV
                     DYKRSYPTNSLTRSHQATTLKRNNTNSSNSSHLSRNQSFGRGDNPPPAPQRVDSIQVH
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ORIGIN

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  Matches  216;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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Qy          1 CCGCCGCCCGCCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3532 CCGCCGCCCGCCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC 3591

Qy         61 CAGGCCGTGACTGTCTCGAGGCAGCCCAGCCTCAACGCCTACAACTCACTGACAAGGTCG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3592 CAGGCCGTGACTGTCTCGAGGCAGCCCAGCCTCAACGCCTACAACTCACTGACAAGGTCG 3651

Qy        121 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3652 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCC 3711

Qy        181 CTTTCCACATCCATGAAGCCCAATGATGCGTGTACA 216
              ||||||||||||||||||||||||||||||||||||
Db       3712 CTTTCCACATCCATGAAGCCCAATGATGCGTGTACA 3747
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Job time : 775.266 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: September 30, 2003, 16:33:04 ; Search time 54.8323 Seconds
(without alignments)
10633.858 Million cell updates/sec

Title: US-09-856-681-3
Perfect score: 216
Sequence: 1 ccgccgcccgccccgcagag.....agcccaatgatgcgtgtaca 216

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	2	216	100.0	1472	21	AAC98050	Human colon cancer
	3	216	100.0	2123	22	AAH13995	Human cDNA sequenc
	4	216	100.0	2227	22	AAK94365	Human full-length
	5	216	100.0	2262	24	ABK34739	Human cDNA for nov
	6	216	100.0	2293	22	AAH15834	Human cDNA sequenc
	7	216	100.0	2306	22	AAH17861	Human cDNA sequenc
	8	216	100.0	2592	23	AAS68253	DNA encoding novel
	9	216	100.0	3039	23	AAS68807	DNA encoding novel
	10	216	100.0	3039	23	AAS89721	DNA encoding novel
	11	216	100.0	3041	22	AAH17625	Human cDNA sequenc
	12	216	100.0	3333	21	AAA93618	Human semaphorin p
	13	216	100.0	3498	21	AAA93617	Human semaphorin p
	14	216	100.0	3550	19	AAV44295	Human secreted pro
	15	216	100.0	3550	22	AAF98469	Human cDNA clone C
	16	216	100.0	3862	21	AAD01233	Human semaphorin 6
	17	216	100.0	4280	25	ABX71103	Novel human cDNA s
	18	216	100.0	6060	22	AAH18729	Human cDNA sequenc
	19	55	25.5	1853	22	AAH15994	Human cDNA sequenc
	20	55	25.5	2581	22	AAH16063	Human cDNA sequenc
	21	55	25.5	3196	24	ABS64382	Human semaphorin-1
	22	55	25.5	3205	24	ABS64380	Human semaphorin 6
	23	55	25.5	3364	24	ABS64384	Human semaphorin-1
	24	55	25.5	3694	22	AAH42597	Nucleotide sequenc
	25	55	25.5	4234	24	ABA00055	CADHP-2 coding seq
	26	55	25.5	6645	25	ABX34714	Human mddt cDNA SE
	27	55	25.5	6767	22	AAL04256	Human reproductive
	28	55	25.5	6773	22	AAL04255	Human reproductive
	29	53.4	24.7	662	22	AAL00809	Human reproductive
c	30	42.8	19.8	575	22	AAH10827	Human cDNA clone (
	31	36.8	17.0	670	22	AAC90703	Human secretory pr
c	32	35.4	16.4	1971	19	AAV58278	Fluorescent calmod
	33	35.2	16.3	936	25	ABT19408	Aspergillus fumiga
	34	35.2	16.3	936	25	ABT21228	Aspergillus fumiga
	35	35.2	16.3	1015	25	ABT18814	Aspergillus fumiga
	36	35.2	16.3	1015	25	ABT20630	Aspergillus fumiga
	37	35.2	16.3	3015	25	ABT18220	Aspergillus fumiga
	38	35.2	16.3	3015	25	ABT20034	Aspergillus fumiga
c	39	35.2	16.3	13987	18	AAT80415	Hybrid srmG/tylG O
c	40	35.2	16.3	43280	18	AAT80413	Tylactone synthase
c	41	34.4	15.9	4403765	22	AAI99683	Mycobacterium tube
c	42	34.4	15.9	4411529	22	AAI99682	Mycobacterium tube
	43	33.4	15.5	5571	25	ABX72218	Human NOVX polynuc
c	44	33.2	15.4	936	25	ABZ71148	S. murayamaensis A
	45	33.2	15.4	2293	24	ABS57346	cDNA encoding huma

ALIGNMENTS

RESULT 1
AAD01234
ID AAD01234 standard; DNA; 216 BP.
XX
AC AAD01234;
XX
DT 04-OCT-2000 (first entry)
XX
DE DNA encoding binding domain of human semaphorin 6A-1.
XX
KW Human; semaphorin 6A-1; (HSA)SEMA6A-1; neuronal development; apoptosis;
KW neuronal regeneration; Ena/VASP protein family; immunomodulatory;
KW gene therapy; diagnostic agent; therapeutic agent; differentiation;
KW cytoskeletal stabilisation; plasticity; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1..216
FT /*tag= a
FT /product= "Binding domain of semaphorin 6A-1"
FT /note= "The binding domain shows homology to Zyxin
FT protein and selectively binds to members of Ena/VASP
FT protein family, especially Evl; the CDS does not
FT include stop codon"
FT /partial
XX
PN WO200031252-A1.
XX
PD 02-JUN-2000.
XX

PF 26-NOV-1999; 99WO-EP09215.
XX
PR 26-NOV-1998; 98EP-0122441.
XX
PA (PLAC) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
XX
PI Behl C, Klostermann A;
XX
DR WPI; 2000-400065/34.
DR P-PSDB; AAY71461.
XX
PT Nucleic acid coding for human semaphorin 6A-1 used as diagnostic agent,
PT therapeutic agent, for modulating immune system, in gene therapy or for
PT effecting differentiation, cytoskeletal stabilization and/or plasticity
PT -
XX
PS Claim 2; Page 21; 53pp; English.
XX
CC The present sequence is a DNA encoding binding domain of transmembranous
CC human semaphorin 6A-1 ((HSA)SEMA6A-1) which is involved in neuronal
CC development and regeneration mechanisms during apoptosis. The binding
CC domain shows homology to Zyxin protein and selectively binds to members
CC of Ena/VASP protein family, especially Evl. (HSA)SEMA6A-1 is a
CC member of protein family displaying secreted or transmembrane-based
CC repulsive guidance cues critically involved in neuronal development.
CC Expression of (HSA)SEMA6A-1 is highest in embryonic brain and
CC kidney and moderate in lung. The present sequence is useful as diagnostic
CC and therapeutic agents, for modulating the immune system, in gene
CC therapy, for effecting differentiation, cytoskeletal stabilisation
CC and plasticity.
XX
SQ Sequence 216 BP; 45 A; 85 C; 51 G; 35 T; 0 other;

Query Match 100.0%; Score 216; DB 21; Length 216;
Best Local Similarity 100.0%; Pred. No. 2e-52;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CCGCCGCCCGCCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC 60

Qy         61 CAGGCCGTGACTGTCTCGAGGCAGCCCAGCCTCAACGCCTACAACTCACTGACAAGGTCG 120
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Db         61 CAGGCCGTGACTGTCTCGAGGCAGCCCAGCCTCAACGCCTACAACTCACTGACAAGGTCG 120

Qy        121 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCC 180
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Db        121 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCC 180

Qy        181 CTTTCCACATCCATGAAGCCCAATGATGCGTGTACA 216
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Db        181 CTTTCCACATCCATGAAGCCCAATGATGCGTGTACA 216
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RESULT 2
AAC98050
ID AAC98050 standard; cDNA; 1472 BP.
XX
AC AAC98050;
XX
DT 09-MAR-2001 (first entry)
XX
DE Human colon cancer antigen nucleotide sequence SEQ ID NO:60.
XX
KW Human; colon cancer; colon cancer antigen; diagnosis; detection;
KW identification; cytostatic; cardioactive; neuroprotective; vulnerary;
KW immunomodulatory; muscular; gynaecological; gastrointestinal;
KW nephrotropic; antiinfective; antibacterial; gene therapy; wound;
KW neural disorder; immune system disorder; muscular disorder;
KW reproductive disorder; gastrointestinal disorder; renal disorder;
KW infectious disease; cardiovascular disorder; ss.
XX
OS Homo sapiens.
XX
PN WO200055351-A1.
XX
PD 21-SEP-2000.
XX
PF 08-MAR-2000; 2000WO-US05883.
XX
PR 12-MAR-1999; 99US-0124270.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Ruben SM;
XX
DR WPI; 2000-587534/55.
DR P-PSDB; AAB53293.
XX
PT Colon cancer associated gene sequences, referred to as colon cancer
PT antigens, useful for the treatment, prevention, and diagnosis of colon
PT disorders such as colon cancer -
XX
PS Claim 1; Page 510-511; 2104pp; English.
XX
CC AAC97991 to AAC98763 encode the human colon cancer associated proteins,
CC called human colon cancer antigens, given in AAB53234 to AAB54006. The
CC human colon cancer antigens can have cytostatic, cardioactive, muscular;
CC neuroprotective, immunomodulatory, gynaecological, gastrointestinal,
CC vulnerary, nephrotropic, antiinfective and antibacterial activities, and
CC can be used in gene therapy. The colon cancer antigen polynucleotides,
CC proteins and antibodies to the proteins are useful for the prevention,
CC treatment and diagnosis of colon disorders, such as colon cancer. The
CC polynucleotides may be used in diagnostics and research, such as for
CC chromosome identification, and as hybridisation probes. The proteins
CC may also be used to prevent diseases such as neural disorders, immune
CC system disorders, muscular disorders, reproductive disorders,
CC gastrointestinal disorders, wounds, renal disorders, infectious
CC diseases, and cardiovascular disorders. AAC98764 to AAC98772 and
CC AAB54007 represent sequences used in the exemplification of the present
CC invention.
XX
SQ Sequence 1472 BP; 437 A; 431 C; 299 G; 301 T; 4 other;

Query Match 100.0%; Score 216; DB 21; Length 1472;
Best Local Similarity 100.0%; Pred. No. 3.2e-52;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 CCGCCGCCCGCCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        372 CCGCCGCCCGCCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC 431

Qy         61 CAGGCCGTGACTGTCTCGAGGCAGCCCAGCCTCAACGCCTACAACTCACTGACAAGGTCG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        432 CAGGCCGTGACTGTCTCGAGGCAGCCCAGCCTCAACGCCTACAACTCACTGACAAGGTCG 491

Qy        121 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        492 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCC 551

Qy        181 CTTTCCACATCCATGAAGCCCAATGATGCGTGTACA 216
              |||||||||||||||||||||||||||||||||||
Db        552 CTTTCCACATCCATGAAGCCCAATGATGCGTGTACA 587
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RESULT 3
AAH13995
ID AAH13995 standard; cDNA; 2123 BP.
XX
AC AAH13995;
XX
DT 26-JUN-2001 (first entry)
XX
DE Human cDNA sequence SEQ ID NO:11072.
XX
KW Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.

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XX
OS   Homo sapiens.
XX
PN   EP1074617-A2.
XX
PD   07-FEB-2001.
XX
PF   28-JUL-2000; 2000EP-0116126.
XX
PR   29-JUL-1999;   99JP-0248036.
PR   27-AUG-1999;   99JP-0300253.
PR   11-JAN-2000; 2000JP-0118776.
PR   02-MAY-2000; 2000JP-0183767.
PR   09-JUN-2000; 2000JP-0241899.
XX
PA   (HELI-) HELIX RES INST.
XX
PI   Ota T,  Isogai T,  Nishikawa T,  Hayashi K,  Saito K,  Yamamoto J;
PI   Ishii S,  Sugiyama T,  Wakamatsu A,  Nagai K,  Otsuki T;
XX
DR   WPI; 2001-318749/34.
XX
PT   Primer sets for synthesizing polynucleotides, particularly the 5602
PT   full-length cDNAs defined in the specification, and for the detection
PT   and/or diagnosis of the abnormality of the proteins encoded by the
PT   full-length cDNAs -
XX
PS   Claim 8; SEQ ID 11072; 2537pp + CD ROM; English.
XX
CC   The present invention describes primer sets for synthesising 5602
CC   full-length cDNAs defined in the specification. Where a primer set
CC   comprises: (a) an oligo-dT primer and an oligonucleotide complementary
CC   to the complementary strand of a polynucleotide which comprises one of
CC   the 5602 nucleotide sequences defined in the specification, where the
CC   oligonucleotide comprises at least 15 nucleotides; or (b) a combination
CC   of an oligonucleotide comprising a sequence complementary to the
CC   complementary strand of a polynucleotide which comprises a 5'-end
CC   sequence and an oligonucleotide comprising a sequence complementary to a
CC   polynucleotide which comprises a 3'-end sequence, where the
CC   oligonucleotide comprises at least 15 nucleotides and the combination of
CC   the 5'-end sequence/3'-end sequence is selected from those defined in
CC   the specification. The primer sets can be used in antisense therapy and
CC   in gene therapy. The primers are useful for synthesising polynucleotides,
CC   particularly full-length cDNAs. The primers are also useful for the
CC   detection and/or diagnosis of the abnormality of the proteins encoded by
CC   the full-length cDNAs. The primers allow obtaining of the full-length
CC   cDNAs easily without any specialised methods. AAH03166 to AAH13628 and
CC   AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to
CC   AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632
CC   represent oligonucleotides, all of which are used in the exemplification
CC   of the present invention.
XX
SQ   Sequence 2123 BP; 550 A; 664 C; 528 G; 381 T; 0 other;

  Query Match             100.0%;  Score 216;  DB 22;  Length 2123;
  Best Local Similarity   100.0%;  Pred. No. 3.5e-52;
  Matches  216;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CCGCCGCCCGCCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC 60
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Db       1432 CCGCCGCCCGCCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC 1491

Qy         61 CAGGCCGTGACTGTCTCGAGGCAGCCCAGCCTCAACGCCTACAACTCACTGACAAGGTCG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1492 CAGGCCGTGACTGTCTCGAGGCAGCCCAGCCTCAACGCCTACAACTCACTGACAAGGTCG 1551

Qy        121 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1552 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCC 1611

Qy        181 CTTTCCACATCCATGAAGCCCAATGATGCGTGTACA 216
              |||||||||||||||||||||||||||||||||||||
Db       1612 CTTTCCACATCCATGAAGCCCAATGATGCGTGTACA 1647


RESULT 4
AAK94365
ID   AAK94365 standard; cDNA; 2227 BP.
XX
AC   AAK94365;
XX
DT   06-NOV-2001  (first entry)
XX
DE   Human full-length cDNA, SEQ ID NO: 3087.
XX
KW   Human; full length cDNA; cDNA synthesis; oligo-capping; ss.
XX
OS   Homo sapiens.
XX
PN   EP1130094-A2.
XX
PD   05-SEP-2001.
XX
PF   07-JUL-2000; 2000EP-0114089.
XX
PR   08-JUL-1999;   99JP-0194486.
PR   11-JAN-2000; 2000JP-0118774.
PR   02-MAY-2000; 2000JP-0183765.
XX
PA   (HELI-) HELIX RES INST.
XX
PI   Ota T,  Nishikawa T,  Isogai T,  Hayashi K,  Ishii S,  Kawai Y;
PI   Wakamatsu A,  Sugiyama T,  Nagai K,  Kojima S,  Otsuki T,  Koga H;
XX
DR   WPI; 2001-524255/58.
DR   P-PSDB; AAM93444.
XX
PT   830 Primers useful for synthesizing full length cDNA clones and their
PT   use in genetic manipulation -
XX
PS   Claim 8; SEQ ID NO 3087; 1380pp + sequence listing; English.
XX
CC   The invention relates to primers for synthesising full length cDNA
CC   clones. 830 cDNA molecules encoding a human protein have been
CC   isolated and nucleotide sequences of 5'- and 3'-ends of the cDNA
CC   molecules have been determined. Primers for synthesising the full length
CC   cDNA are useful for clarifying the function of the protein encoded by
CC   the cDNA. The full length clones were obtained by construction of full
CC   length enriched cDNA libraries that were synthesised by the oligo-capping
CC   method. The primers enable the production of the full length cDNA easily
CC   without any special methods. The present sequence is a full length
CC   human cDNA of the invention.
CC   Note: The sequence data for this patent did not form part of the printed
CC   specification, but was obtained in CD-ROM format directly from EPO.
XX
SQ   Sequence 2227 BP; 567 A; 700 C; 560 G; 400 T; 0 other;

  Query Match             100.0%;  Score 216;  DB 22;  Length 2227;
  Best Local Similarity   100.0%;  Pred. No. 3.6e-52;
  Matches  216;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CCGCCGCCCGCCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1526 CCGCCGCCCGCCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC 1585

Qy         61 CAGGCCGTGACTGTCTCGAGGCAGCCCAGCCTCAACGCCTACAACTCACTGACAAGGTCG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1586 CAGGCCGTGACTGTCTCGAGGCAGCCCAGCCTCAACGCCTACAACTCACTGACAAGGTCG 1645

Qy        121 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1646 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCC 1705

Qy        181 CTTTCCACATCCATGAAGCCCAATGATGCGTGTACA 216
              |||||||||||||||||||||||||||||||||||||
Db       1706 CTTTCCACATCCATGAAGCCCAATGATGCGTGTACA 1741
```

```
RESULT 5
ABK34739
ID   ABK34739 standard; cDNA; 2262 BP.
XX
AC   ABK34739;
XX
DT   08-MAY-2002  (first entry)
XX
DE   Human cDNA for novel secreted protein, SEQ ID 508.
XX
KW   Human; ss; gene; secreted protein; immune deficiency; viral infection;
KW   bacterial infection; fungal infection; autoimmune disorder; burn;
KW   rheumatoid arthritis; multiple sclerosis; autoimmune thyroiditis;
KW   diabetes; allergy; asthma; neurodegenerative disease; Crohn's disease;
KW   Alzheimer's disease; Parkinson's disease; liver fibrosis; tumour;
KW   coagulation disorder; haemophilia; inflammatory disorder; ulcer;
KW   tissue regeneration; wound healing; haematopoiesis; myeloid deficiency;
KW   lymphoid cell deficiency.
XX
OS   Homo sapiens.
XX
PN   WO200177290-A2.
XX
PD   18-OCT-2001.
XX
PF   29-MAR-2001; 2001WO-US10295.
XX
PR   06-APR-2000; 2000US-194941P.
XX
PA   (GEMY ) GENETICS INST INC.
XX
PI   Wong GG, Clark HF, Fechtel K, Agostino MJ, Howes SH, Resnick RJ;
PI   Gulukota K, Graham JR;
XX
DR   WPI; 2002-179323/23.
XX
PT   Six hundred and twenty five polynucleotides derived from a variety of
PT   human tissue sources which encode secreted proteins, useful for
PT   treating immune deficiencies and disorders such as autoimmune disorders
PT   -
XX
PS   Claim 1; Page 272; 339pp; English.
XX
CC   The invention relates to 625 polynucleotides which have been derived from
CC   a variety of human tissue sources and which encode novel secreted
CC   proteins, their complements and sequences that hybridise to them.
CC   Also included are a vector comprising the polynucleotide, a host cell
CC   transformed with the vector, the proteins encoded by the
CC   polynucleotides, antibodies that bind to the proteins and identification
CC   of modulators of the proteins or the expression of the polynucleotide.
CC   The polynucleotides can be used as probes for the identification
CC   and isolation of full length cDNA and genomic DNA. The polynucleotides
CC   and proteins can also be used as nutritional supplements. The protein
CC   is useful in the treatment of various immune deficiencies and disorders
CC   such as viral infections, bacterial infections, fungal infections,
CC   autoimmune disorders (e.g. rheumatoid arthritis, multiple sclerosis,
CC   autoimmune thyroiditis and diabetes) and allergic reactions and
CC   conditions (e.g. asthma). They are also useful for treating
CC   neurodegenerative diseases (e.g. Alzheimer's disease, Parkinson's
CC   disease), liver fibrosis, coagulation disorders (e.g. haemophilia),
CC   inflammatory disorders (e.g. Crohn's disease) and tumours. They are also
CC   useful for tissue regeneration, for wound healing and in the treatment
CC   of burns, incisions and ulcers. The proteins are also useful for
CC   regulating haematopoiesis, for treating myeloid or lymphoid cell
CC   deficiencies. The present sequence is one of the 625 cDNA sequences
CC   encoding a secreted protein.
XX
SQ   Sequence 2262 BP; 604 A; 695 C; 522 G; 441 T; 0 other;

  Query Match             100.0%;  Score 216;  DB 24;  Length 2262;
  Best Local Similarity   100.0%;  Pred. No. 3.6e-52;
  Matches  216;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CCGCCGCCCGCCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1184 CCGCCGCCCGCCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC 1243

Qy         61 CAGGCCGTGACTGTCTCGAGGCAGCCCAGCCTCAACGCCTACAACTCACTGACAAGGTCG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1244 CAGGCCGTGACTGTCTCGAGGCAGCCCAGCCTCAACGCCTACAACTCACTGACAAGGTCG 1303

Qy        121 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1304 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCC 1363

Qy        181 CTTTCCACATCCATGAAGCCCAATGATGCGTGTACA 216
              ||||||||||||||||||||||||||||||||||||
Db       1364 CTTTCCACATCCATGAAGCCCAATGATGCGTGTACA 1399


RESULT 6
AAH15834
ID   AAH15834 standard; cDNA; 2293 BP.
XX
AC   AAH15834;
XX
DT   26-JUN-2001  (first entry)
XX
DE   Human cDNA sequence SEQ ID NO:14327.
XX
KW   Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.
XX
OS   Homo sapiens.
XX
PN   EP1074617-A2.
XX
PD   07-FEB-2001.
XX
PF   28-JUL-2000; 2000EP-0116126.
XX
PR   29-JUL-1999;   99JP-0248036.
PR   27-AUG-1999;   99JP-0300253.
PR   11-JAN-2000; 2000JP-0118776.
PR   02-MAY-2000; 2000JP-0183767.
PR   09-JUN-2000; 2000JP-0241899.
XX
PA   (HELI-) HELIX RES INST.
XX
PI   Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
PI   Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
XX
DR   WPI; 2001-318749/34.
XX
PT   Primer sets for synthesizing polynucleotides, particularly the 5602
PT   full-length cDNAs defined in the specification, and for the detection
PT   and/or diagnosis of the abnormality of the proteins encoded by the
PT   full-length cDNAs -
XX
PS   Claim 8; SEQ ID 14327; 2537pp + CD ROM; English.
XX
CC   The present invention describes primer sets for synthesising 5602
CC   full-length cDNAs defined in the specification. Where a primer set
CC   comprises: (a) an oligo-dT primer and an oligonucleotide complementary
CC   to the complementary strand of a polynucleotide which comprises one of
CC   the 5602 nucleotide sequences defined in the specification, where the
CC   oligonucleotide comprises at least 15 nucleotides; or (b) a combination
CC   of an oligonucleotide comprising a sequence complementary to the
CC   complementary strand of a polynucleotide which comprises a 5'-end
CC   sequence and an oligonucleotide comprising a sequence complementary to a
CC   polynucleotide which comprises a 3'-end sequence, where the
CC   oligonucleotide comprises at least 15 nucleotides and the combination of
CC   the 5'-end sequence/3'-end sequence is selected from those defined in
CC   the specification. The primer sets can be used in antisense therapy and
CC   in gene therapy. The primers are useful for synthesising polynucleotides,
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CC   particularly full-length cDNAs. The primers are also useful for the
CC   detection and/or diagnosis of the abnormality of the proteins encoded by
CC   the full-length cDNAs. The primers allow obtaining of the full-length
CC   cDNAs easily without any specialised methods. AAH03166 to AAH13628 and
CC   AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to
CC   AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632
CC   represent oligonucleotides, all of which are used in the exemplification
CC   of the present invention.
XX
SQ   Sequence 2293 BP; 579 A; 713 C; 581 G; 420 T; 0 other;

  Query Match           100.0%;  Score 216;  DB 22;  Length 2293;
  Best Local Similarity  100.0%;  Pred. No. 3.6e-52;
  Matches  216;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CCGCCGCCCCGCCCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1608 CCGCCGCCCGCCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC 1667

Qy         61 CAGGCCGTGACTGTCTCGAGGCAGCCCAGCCTCAACGCCTACAACTCACTGACAAGGTCG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1668 CAGGCCGTGACTGTCTCGAGGCAGCCCAGCCTCAACGCCTACAACTCACTGACAAGGTCG 1727

Qy        121 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1728 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCC 1787

Qy        181 CTTTCCACATCCATGAAGCCCAATGATGCGTGTACA 216
              |||||||||||||||||||||||||||||||||||
Db       1788 CTTTCCACATCCATGAAGCCCAATGATGCGTGTACA 1823


RESULT 7
AAH17861
ID   AAH17861 standard; cDNA; 2306 BP.
XX
AC   AAH17861;
XX
DT   26-JUN-2001  (first entry)
XX
DE   Human cDNA sequence SEQ ID NO:17567.
XX
KW   Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.
XX
OS   Homo sapiens.
XX
PN   EP1074617-A2.
XX
PD   07-FEB-2001.
XX
PF   28-JUL-2000; 2000EP-0116126.
XX
PR   29-JUL-1999;   99JP-0248036.
PR   27-AUG-1999;   99JP-0300253.
PR   11-JAN-2000; 2000JP-0118776.
PR   02-MAY-2000; 2000JP-0183767.
PR   09-JUN-2000; 2000JP-0241899.
XX
PA   (HELI-) HELIX RES INST.
XX
PI   Ota T,  Isogai T,  Nishikawa T,  Hayashi K,  Saito K,  Yamamoto J;
PI   Ishii S,  Sugiyama T,  Wakamatsu A,  Nagai K,  Otsuki T;
XX
DR   WPI; 2001-318749/34.
XX
PT   Primer sets for synthesizing polynucleotides, particularly the 5602
PT   full-length cDNAs defined in the specification, and for the detection
PT   and/or diagnosis of the abnormality of the proteins encoded by the
PT   full-length cDNAs -
XX
PS   Claim 8; SEQ ID 17567; 2537pp + CD ROM; English.
XX
CC   The present invention describes primer sets for synthesising 5602
CC   full-length cDNAs defined in the specification. Where a primer set
CC   comprises: (a) an oligo-dT primer and an oligonucleotide complementary
CC   to the complementary strand of a polynucleotide which comprises one of
CC   the 5602 nucleotide sequences defined in the specification, where the
CC   oligonucleotide comprises at least 15 nucleotides; or (b) a combination
CC   of an oligonucleotide comprising a sequence complementary to the
CC   complementary strand of a polynucleotide which comprises a 5'-end
CC   sequence and an oligonucleotide comprising a sequence complementary to a
CC   polynucleotide which comprises a 3'-end sequence, where the
CC   oligonucleotide comprises at least 15 nucleotides and the combination of
CC   the 5'-end sequence/3'-end sequence is selected from those defined in
CC   the specification. The primer sets can be used in antisense therapy and
CC   in gene therapy. The primers are useful for synthesising polynucleotides,
CC   particularly full-length cDNAs. The primers are also useful for the
CC   detection and/or diagnosis of the abnormality of the proteins encoded by
CC   the full-length cDNAs. The primers allow obtaining of the full-length
CC   cDNAs easily without any specialised methods. AAH03166 to AAH13628 and
CC   AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to
CC   AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632
CC   represent oligonucleotides, all of which are used in the exemplification
CC   of the present invention.
XX
SQ   Sequence 2306 BP; 579 A; 739 C; 577 G; 411 T; 0 other;

  Query Match           100.0%;  Score 216;  DB 22;  Length 2306;
  Best Local Similarity  100.0%;  Pred. No. 3.6e-52;
  Matches  216;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CCGCCGCCCGCCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1615 CCGCCGCCCGCCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC 1674

Qy         61 CAGGCCGTGACTGTCTCGAGGCAGCCCAGCCTCAACGCCTACAACTCACTGACAAGGTCG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1675 CAGGCCGTGACTGTCTCGAGGCAGCCCAGCCTCAACGCCTACAACTCACTGACAAGGTCG 1734

Qy        121 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1735 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCC 1794

Qy        181 CTTTCCACATCCATGAAGCCCAATGATGCGTGTACA 216
              |||||||||||||||||||||||||||||||||||
Db       1795 CTTTCCACATCCATGAAGCCCAATGATGCGTGTACA 1830


RESULT 8
AAS68253
ID   AAS68253 standard; cDNA; 2592 BP.
XX
AC   AAS68253;
XX
DT   13-FEB-2002  (first entry)
XX
DE   DNA encoding novel human diagnostic protein #4057.
XX
KW   Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW   food supplement; medical imaging; diagnostic; genetic disorder; ss.
XX
OS   Homo sapiens.
XX
PN   WO200175067-A2.
XX
PD   11-OCT-2001.
XX
PF   30-MAR-2001; 2001WO-US08631.
XX
PR   31-MAR-2000; 2000US-0540217.
PR   23-AUG-2000; 2000US-0649167.
XX
PA   (HYSE-) HYSEQ INC.
XX
PI   Drmanac RT,  Liu C,  Tang YT;
XX
```

```
DR   WPI; 2001-639362/73.
DR   P-PSDB; ABG04066.
XX
PT   New isolated polynucleotide and encoded polypeptides, useful in
PT   diagnostics, forensics, gene mapping, identification of mutations
PT   responsible for genetic disorders or other traits and to assess
PT   biodiversity -
XX
PS   Claim 1; SEQ ID No 4057; 103pp; English.
XX
CC   The invention relates to isolated polynucleotide (I) and
CC   polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC   polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC   and gene mapping, and in recombinant production of (II). The
CC   polynucleotides are also used in diagnostics as expressed sequence tags
CC   for identifying expressed genes. (I) is useful in gene therapy techniques
CC   to restore normal activity of (II) or to treat disease states involving
CC   (II). (II) is useful for generating antibodies against it, detecting or
CC   quantitating a polypeptide in tissue, as molecular weight markers and as
CC   a food supplement. (II) and its binding partners are useful in medical
CC   imaging of sites expressing (II). (I) and (II) are useful for treating
CC   disorders involving aberrant protein expression or biological activity.
CC   The polypeptide and polynucleotide sequences have applications in
CC   diagnostics, forensics, gene mapping, identification of mutations
CC   responsible for genetic disorders or other traits to assess biodiversity
CC   and to produce other types of data and products dependent on DNA and
CC   amino acid sequences. AAS64197-AAS94564 represent novel human
CC   diagnostic coding sequences of the invention.
CC   Note: The sequence data for this patent did not appear in the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence 2592 BP; 655 A; 754 C; 659 G; 524 T; 0 other;

  Query Match            100.0%;  Score 216;  DB 23;  Length 2592;
  Best Local Similarity  100.0%;  Pred. No. 3.7e-52;
  Matches  216;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CCGCCGCCCGCCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2374 CCGCCGCCCGCCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC 2433

Qy         61 CAGGCCGTGACTGTCTCGAGGCAGCCCAGCCTCAACGCCTACAACTCACTGACAAGGTCG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2434 CAGGCCGTGACTGTCTCGAGGCAGCCCAGCCTCAACGCCTACAACTCACTGACAAGGTCG 2493

Qy        121 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2494 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCC 2553

Qy        181 CTTTCCACATCCATGAAGCCCAATGATGCGTGTACA 216
              |||||||||||||||||||||||||||||||||||
Db       2554 CTTTCCACATCCATGAAGCCCAATGATGCGTGTACA 2589


RESULT 9
AAS68807
ID   AAS68807 standard; cDNA; 3039 BP.
XX
AC   AAS68807;
XX
DT   13-FEB-2002  (first entry)
XX
DE   DNA encoding novel human diagnostic protein #4611.
XX
KW   Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW   food supplement; medical imaging; diagnostic; genetic disorder; ss.
XX
OS   Homo sapiens.
XX
PN   WO200175067-A2.
XX
PD   11-OCT-2001.
XX
PF   30-MAR-2001; 2001WO-US08631.
XX
PR   31-MAR-2000; 2000US-0540217.
PR   23-AUG-2000; 2000US-0649167.
XX
PA   (HYSE-) HYSEQ INC.
XX
PI   Drmanac RT,  Liu C,  Tang YT;
XX
DR   WPI; 2001-639362/73.
DR   P-PSDB; ABG04620.
XX
PT   New isolated polynucleotide and encoded polypeptides, useful in
PT   diagnostics, forensics, gene mapping, identification of mutations
PT   responsible for genetic disorders or other traits and to assess
PT   biodiversity -
XX
PS   Claim 1; SEQ ID No 4611; 103pp; English.
XX
CC   The invention relates to isolated polynucleotide (I) and
CC   polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC   polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC   and gene mapping, and in recombinant production of (II). The
CC   polynucleotides are also used in diagnostics as expressed sequence tags
CC   for identifying expressed genes. (I) is useful in gene therapy techniques
CC   to restore normal activity of (II) or to treat disease states involving
CC   (II). (II) is useful for generating antibodies against it, detecting or
CC   quantitating a polypeptide in tissue, as molecular weight markers and as
CC   a food supplement. (II) and its binding partners are useful in medical
CC   imaging of sites expressing (II). (I) and (II) are useful for treating
CC   disorders involving aberrant protein expression or biological activity.
CC   The polypeptide and polynucleotide sequences have applications in
CC   diagnostics, forensics, gene mapping, identification of mutations
CC   responsible for genetic disorders or other traits to assess biodiversity
CC   and to produce other types of data and products dependent on DNA and
CC   amino acid sequences. AAS64197-AAS94564 represent novel human
CC   diagnostic coding sequences of the invention.
CC   Note: The sequence data for this patent did not appear in the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence 3039 BP; 741 A; 869 C; 781 G; 648 T; 0 other;

  Query Match            100.0%;  Score 216;  DB 23;  Length 3039;
  Best Local Similarity  100.0%;  Pred. No. 3.8e-52;
  Matches  216;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CCGCCGCCCGCCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2821 CCGCCGCCCGCCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC 2880

Qy         61 CAGGCCGTGACTGTCTCGAGGCAGCCCAGCCTCAACGCCTACAACTCACTGACAAGGTCG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2881 CAGGCCGTGACTGTCTCGAGGCAGCCCAGCCTCAACGCCTACAACTCACTGACAAGGTCG 2940

Qy        121 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2941 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCC 3000

Qy        181 CTTTCCACATCCATGAAGCCCAATGATGCGTGTACA 216
              |||||||||||||||||||||||||||||||||||
Db       3001 CTTTCCACATCCATGAAGCCCAATGATGCGTGTACA 3036


RESULT 10
AAS89721
ID   AAS89721 standard; cDNA; 3039 BP.
XX
AC   AAS89721;
XX
DT   13-FEB-2002  (first entry)
XX
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```
DE   DNA encoding novel human diagnostic protein #25525.
XX
KW   Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW   food supplement; medical imaging; diagnostic; genetic disorder; ss.
XX
OS   Homo sapiens.
XX
PN   WO200175067-A2.
XX
PD   11-OCT-2001.
XX
PF   30-MAR-2001; 2001WO-US08631.
XX
PR   31-MAR-2000; 2000US-0540217.
PR   23-AUG-2000; 2000US-0649167.
XX
PA   (HYSE-) HYSEQ INC.
XX
PI   Drmanac RT,  Liu C,  Tang YT;
XX
DR   WPI; 2001-639362/73.
DR   P-PSDB; ABG25534.
XX
PT   New isolated polynucleotide and encoded polypeptides, useful in
PT   diagnostics, forensics, gene mapping, identification of mutations
PT   responsible for genetic disorders or other traits and to assess
PT   biodiversity -
XX
PS   Claim 1; SEQ ID No 25525; 103pp; English.
XX
CC   The invention relates to isolated polynucleotide (I) and
CC   polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC   polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC   and gene mapping, and in recombinant production of (II). The
CC   polynucleotides are also used in diagnostics as expressed sequence tags
CC   for identifying expressed genes. (I) is useful in gene therapy techniques
CC   to restore normal activity of (II) or to treat disease states involving
CC   (II). (II) is useful for generating antibodies against it, detecting or
CC   quantitating a polypeptide in tissue, as molecular weight markers and as
CC   a food supplement. (II) and its binding partners are useful in medical
CC   imaging of sites expressing (II). (I) and (II) are useful for treating
CC   disorders involving aberrant protein expression or biological activity.
CC   The polypeptide and polynucleotide sequences have applications in
CC   diagnostics, forensics, gene mapping, identification of mutations
CC   responsible for genetic disorders or other traits to assess biodiversity
CC   and to produce other types of data and products dependent on DNA and
CC   amino acid sequences. AAS64197-AAS94564 represent novel human
CC   diagnostic coding sequences of the invention.
CC   Note: The sequence data for this patent did not appear in the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence 3039 BP; 741 A; 869 C; 781 G; 648 T; 0 other;

  Query Match             100.0%;  Score 216;  DB 23;  Length 3039;
  Best Local Similarity   100.0%;  Pred. No. 3.8e-52;
  Matches  216;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CCGCCGCCCCGCCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2821 CCGCCGCCCCGCCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC 2880

Qy         61 CAGGCCGTGACTGTCTCGAGGCAGCCCAGCCTCAACGCCTACAACTCACTGACAAGGTCG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2881 CAGGCCGTGACTGTCTCGAGGCAGCCCAGCCTCAACGCCTACAACTCACTGACAAGGTCG 2940

Qy        121 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2941 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCC 3000

Qy        181 CTTTCCACATCCATGAAGCCCAATGATGCGTGTACA 216
              |||||||||||||||||||||||||||||||||||||
Db       3001 CTTTCCACATCCATGAAGCCCAATGATGCGTGTACA 3036
```

```
RESULT 11
AAH17625
ID   AAH17625 standard; cDNA; 3041 BP.
XX
AC   AAH17625;
XX
DT   26-JUN-2001  (first entry)
XX
DE   Human cDNA sequence SEQ ID NO:17153.
XX
KW   Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.
XX
OS   Homo sapiens.
XX
PN   EP1074617-A2.
XX
PD   07-FEB-2001.
XX
PF   28-JUL-2000; 2000EP-0116126.
XX
PR   29-JUL-1999;   99JP-0248036.
PR   27-AUG-1999;   99JP-0300253.
PR   11-JAN-2000; 2000JP-0118776.
PR   02-MAY-2000; 2000JP-0183767.
PR   09-JUN-2000; 2000JP-0241899.
XX
PA   (HELI-) HELIX RES INST.
XX
PI   Ota T,  Isogai T,  Nishikawa T,  Hayashi K,  Saito K,  Yamamoto J;
PI   Ishii S,  Sugiyama T,  Wakamatsu A,  Nagai K,  Otsuki T;
XX
DR   WPI; 2001-318749/34.
XX
PT   Primer sets for synthesizing polynucleotides, particularly the 5602
PT   full-length cDNAs defined in the specification, and for the detection
PT   and/or diagnosis of the abnormality of the proteins encoded by the
PT   full-length cDNAs -
XX
PS   Claim 8; SEQ ID 17153; 2537pp + CD ROM; English.
XX
CC   The present invention describes primer sets for synthesising 5602
CC   full-length cDNAs defined in the specification. Where a primer set
CC   comprises: (a) an oligo-dT primer and an oligonucleotide complementary
CC   to the complementary strand of a polynucleotide which comprises one of
CC   the 5602 nucleotide sequences defined in the specification, where the
CC   oligonucleotide comprises at least 15 nucleotides; or (b) a combination
CC   of an oligonucleotide comprising a sequence complementary to the
CC   complementary strand of a polynucleotide which comprises a 5'-end
CC   sequence and an oligonucleotide comprising a sequence complementary to a
CC   polynucleotide which comprises a 3'-end sequence, where the
CC   oligonucleotide comprises at least 15 nucleotides and the combination of
CC   the 5'-end sequence/3'-end sequence is selected from those defined in
CC   the specification. The primer sets can be used in antisense therapy and
CC   in gene therapy. The primers are useful for synthesising polynucleotides,
CC   particularly full-length cDNAs. The primers are also useful for the
CC   detection and/or diagnosis of the abnormality of the proteins encoded by
CC   the full-length cDNAs. The primers allow obtaining of the full-length
CC   cDNAs easily without any specialised methods. AAH03166 to AAH13628 and
CC   AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to
CC   AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632
CC   represent oligonucleotides, all of which are used in the exemplification
CC   of the present invention.
XX
SQ   Sequence 3041 BP; 804 A; 886 C; 714 G; 637 T; 0 other;

  Query Match             100.0%;  Score 216;  DB 22;  Length 3041;
  Best Local Similarity   100.0%;  Pred. No. 3.8e-52;
  Matches  216;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CCGCCGCCCCGCCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db       1966 CCGCCGCCCGCCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC 2025

Qy         61 CAGGCCGTGACTGTCTCGAGGCAGCCCAGCCTCAACGCCTACAACTCACTGACAAGGTCG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2026 CAGGCCGTGACTGTCTCGAGGCAGCCCAGCCTCAACGCCTACAACTCACTGACAAGGTCG 2085

Qy        121 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2086 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCC 2145

Qy        181 CTTTCCACATCCATGAAGCCCAATGATGCGTGTACA 216
              |||||||||||||||||||||||||||||||||||
Db       2146 CTTTCCACATCCATGAAGCCCAATGATGCGTGTACA 2181
```

RESULT 12
AAA93618
ID AAA93618 standard; DNA; 3333 BP.
XX
AC AAA93618;
XX
DT 16-JAN-2001 (first entry)
XX
DE Human semaphorin protein-like splice variant SECX 2864933-2 DNA.
XX
KW SECX protein; human; secreted; membrane-associated; cancer;
KW proliferation regulator; differentiation regulator; non-malignant tumour;
KW immune disorder; autoimmune disease; transplant rejection; allergy; AIDS;
KW infection; inflammatory disorder; arthritis; haematopoietic disorder;
KW skin disorder; cardiovascular disorder; atherosclerosis; restenosis;
KW neurological disease; Alzheimer's disease; trauma; wounding;
KW spinal cord injury; skeletal disorder; cytostatic; immunosuppressive;
KW anti-HIV; antiinflammatory; antiarthritic; antiarteriosclerotic;
KW neuroprotective; vulnerary; antiallergic; antimicrobial; cardiant;
KW dermatological; gene therapy; ds.
XX
OS Homo sapiens.
XX
PN WO200053742-A2.
XX
PD 14-SEP-2000.
XX
PF 09-MAR-2000; 2000WO-US06280.
XX
PR 09-MAR-1999; 99US-0123667.
PR 08-MAR-2000; 2000US-0123667.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Shimkets RA;
XX
DR WPI; 2000-594318/56.
DR P-PSDB; AAB23031.
XX
PT Novel human membrane associated or secreted polypeptides and
PT polynucleotides useful for diagnosis, prevention and treatment of
PT pathological states such as cancer, immune, cardiovascular and
PT neurological disorders -
XX
PS Claim 3; Fig 3; 151pp; English.
XX
CC Sequences AAA93616-A93631 and AAA93673-A93676 represent nucleic acids
CC which encode human SECX proteins (AAB23029-B23048). The SECX proteins
CC of the invention are either secreted or membrane-associated proteins
CC and act as regulator of cellular proliferation and differentiation. SECX
CC proteins or nucleotides are useful for diagnosing the presence of, or
CC predisposition to, a disease associated with altered levels of SECX
CC proteins and nucleotides. The SECX proteins are also useful to screen
CC compounds that modulate SECX activity or expression. The interaction of
CC a SECX protein with other cellular proteins may be useful to modulate
CC the activity of a partner protein, cellular proliferation, cellular
CC differentiation and cell survival. SECX nucleotides are useful for the
CC recombinant expression of SECX protein, and may be used detect SECX mRNA
CC or genetic lesions in the SECX gene. They may also be used to modulate
CC SECX expression (e.g., using antisense oligonucleotides). SECX nucleic
CC acid sequences are also useful for identifying a cell or tissue type in
CC a biological sample, and in forensic biology. SECX primers or probes are
CC useful for detecting the presence of SECX nucleotides and for screening
CC tissue cultures for contamination. Diseases that may be treated or
CC prevented using SECX proteins or nucleotides include cancer (e.g.,
CC colorectal carcinoma, prostate cancer), benign tumours, immune disorders
CC (including autoimmune diseases, transplant rejection, allergies, AIDS),
CC infections, inflammatory disorders, arthritis, haematopoietic disorders,
CC skin disorders, cardiovascular disorders, atherosclerosis, restenosis,
CC neurological diseases (e.g., Alzheimer's disease), trauma (e.g.,
CC surgical or traumatic wounds, spinal cord injury), and skeletal
CC disorders.
XX
SQ Sequence 3333 BP; 874 A; 921 C; 845 G; 692 T; 1 other;

```
  Query Match             100.0%;  Score 216;  DB 21;  Length 3333;
  Best Local Similarity   100.0%;  Pred. No. 3.9e-52;
  Matches  216;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CCGCCGCCCGCCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2925 CCGCCGCCCGCCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC 2984

Qy         61 CAGGCCGTGACTGTCTCGAGGCAGCCCAGCCTCAACGCCTACAACTCACTGACAAGGTCG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2985 CAGGCCGTGACTGTCTCGAGGCAGCCCAGCCTCAACGCCTACAACTCACTGACAAGGTCG 3044

Qy        121 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3045 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCC 3104

Qy        181 CTTTCCACATCCATGAAGCCCAATGATGCGTGTACA 216
              |||||||||||||||||||||||||||||||||||
Db       3105 CTTTCCACATCCATGAAGCCCAATGATGCGTGTACA 3140
```

RESULT 13
AAA93617
ID AAA93617 standard; DNA; 3498 BP.
XX
AC AAA93617;
XX
DT 16-JAN-2001 (first entry)
XX
DE Human semaphorin protein-like splice variant SECX 2864933-1 DNA.
XX
KW SECX protein; human; secreted; membrane-associated; cancer;
KW proliferation regulator; differentiation regulator; non-malignant tumour;
KW immune disorder; autoimmune disease; transplant rejection; allergy; AIDS;
KW infection; inflammatory disorder; arthritis; haematopoietic disorder;
KW skin disorder; cardiovascular disorder; atherosclerosis; restenosis;
KW neurological disease; Alzheimer's disease; trauma; wounding;
KW spinal cord injury; skeletal disorder; cytostatic; immunosuppressive;
KW anti-HIV; antiinflammatory; antiarthritic; antiarteriosclerotic;
KW neuroprotective; vulnerary; antiallergic; antimicrobial; cardiant;
KW dermatological; gene therapy; ds.
XX
OS Homo sapiens.
XX
PN WO200053742-A2.
XX
PD 14-SEP-2000.
XX
PF 09-MAR-2000; 2000WO-US06280.
XX
PR 09-MAR-1999; 99US-0123667.
PR 08-MAR-2000; 2000US-0123667.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Shimkets RA;

```
XX
DR   WPI; 2000-594318/56.
DR   P-PSDB; AAB23030.
XX
PT   Novel human membrane associated or secreted polypeptides and
PT   polynucleotides useful for diagnosis, prevention and treatment of
PT   pathological states such as cancer, immune, cardiovascular and
PT   neurological disorders -
XX
PS   Claim 3; Fig 2; 151pp; English.
XX
CC   Sequences AAA93616-A93631 and AAA93673-A93676 represent nucleic acids
CC   which encode human SECX proteins (AAB23029-B23048). The SECX proteins
CC   of the invention are either secreted or membrane-associated proteins
CC   and act as regulator of cellular proliferation and differentiation. SECX
CC   proteins or nucleotides are useful for diagnosing the presence of, or
CC   predisposition to, a disease associated with altered levels of SECX
CC   proteins and nucleotides. The SECX proteins are also useful to screen
CC   compounds that modulate SECX activity or expression. The interaction of
CC   a SECX protein with other cellular proteins may be useful to modulate
CC   the activity of a partner protein, cellular proliferation, cellular
CC   differentiation and cell survival. SECX nucleotides are useful for the
CC   recombinant expression of SECX protein, and may be used detect SECX mRNA
CC   or genetic lesions in the SECX gene. They may also be used to modulate
CC   SECX expression (e.g., using antisense oligonucleotides). SECX nucleic
CC   acid sequences are also useful for identifying a cell or tissue type in
CC   a biological sample, and in forensic biology. SECX primers or probes are
CC   useful for detecting the presence of SECX nucleotides and for screening
CC   tissue cultures for contamination. Diseases that may be treated or
CC   prevented using SECX proteins or nucleotides include cancer (e.g.,
CC   colorectal carcinoma, prostate cancer), benign tumours, immune disorders
CC   (including autoimmune diseases, transplant rejection, allergies, AIDS),
CC   infections, inflammatory disorders, arthritis, haematopoietic disorders,
CC   skin disorders, cardiovascular disorders, atherosclerosis, restenosis,
CC   neurological diseases (e.g., Alzheimer's disease), trauma (e.g.,
CC   surgical or traumatic wounds, spinal cord injury), and skeletal
CC   disorders.
XX
SQ   Sequence 3498 BP; 917 A; 966 C; 889 G; 725 T; 1 other;

  Query Match             100.0%;  Score 216;  DB 21;  Length 3498;
  Best Local Similarity   100.0%;  Pred. No. 4e-52;
  Matches  216;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CCGCCGCCCGCCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3090 CCGCCGCCCGCCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC 3149

Qy         61 CAGGCCGTGACTGTCTCGAGGCAGCCCAGCCTCAACGCCTACAACTCACTGACAAGGTCG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3150 CAGGCCGTGACTGTCTCGAGGCAGCCCAGCCTCAACGCCTACAACTCACTGACAAGGTCG 3209

Qy        121 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3210 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCC 3269

Qy        181 CTTTCCACATCCATGAAGCCCAATGATGCGTGTACA 216
              ||||||||||||||||||||||||||||||||||||
Db       3270 CTTTCCACATCCATGAAGCCCAATGATGCGTGTACA 3305


RESULT 14
AAV44295
ID   AAV44295 standard; cDNA; 3550 BP.
XX
AC   AAV44295;
XX
DT   06-OCT-1998  (first entry)
XX
DE   Human secreted protein clone CJ145_1 cDNA.
XX
KW   Secreted protein; human fetal brain; nutrition; cytokine; stimulant;
KW   cell proliferation; differentiation; immune system; suppressor; ligand;
KW   regulator; hematopoiesis; tissue growth; activin; inhibin; haemostatic;
KW   chemotaxis; chemokinetic; thrombosis; receptor; cadherin; tumour;
KW   anti-inflammatory; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             126..3053
FT                   /*tag= a
FT                   /product= secreted protein
FT                   /note= "isolated from clone CJ145_1"
XX
PN   WO9827205-A2.
XX
PD   25-JUN-1998.
XX
PF   17-DEC-1997;   97WO-US23330.
XX
PR   16-DEC-1997;   97US-0991872.
PR   18-DEC-1996;   96US-0769192.
PR   13-JAN-1997;   97US-0783401.
XX
PA   (GEMY ) GENETICS INST INC.
XX
PI   Agostino MJ,  Jacobs K,  Lavallie ER,  McCoy JM,  Merberg D;
PI   Racie LA,  Spaulding V,  Treacy M;
XX
DR   WPI; 1998-362774/31.
DR   P-PSDB; AAW64221.
XX
PT   New polynucleotides and secreted proteins - obtained from human
PT   foetal brain, human adult testes, human adult brain and human adult
PT   salivary gland cDNA libraries
XX
PS   Claim 17a; Page 69-71; 110pp; English.
XX
CC   This sequence encodes a novel secreted protein from clone CJ145_1
CC   isolated from a human fetal brain cDNA library. This protein has
CC   applications for nutritional use, cytokine and cell
CC   proliferation/differentiation activity, immune stimulating or
CC   suppressing activity, hematopoiesis regulating activity, tissue growth
CC   activity, activin/inhibin activity, chemotactic/chemokinetic activity,
CC   haemostatic and thrombotic activity, receptor/ligand activity,
CC   anti-inflammatory activity, cadherin/tumour invasion suppressor activity,
CC   tumour inhibition activity and other activities.
XX
SQ   Sequence 3550 BP; 957 A; 994 C; 856 G; 742 T; 1 other;

  Query Match             100.0%;  Score 216;  DB 19;  Length 3550;
  Best Local Similarity   100.0%;  Pred. No. 4e-52;
  Matches  216;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CCGCCGCCCGCCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2835 CCGCCGCCCGCCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC 2894

Qy         61 CAGGCCGTGACTGTCTCGAGGCAGCCCAGCCTCAACGCCTACAACTCACTGACAAGGTCG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2895 CAGGCCGTGACTGTCTCGAGGCAGCCCAGCCTCAACGCCTACAACTCACTGACAAGGTCG 2954

Qy        121 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2955 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCC 3014

Qy        181 CTTTCCACATCCATGAAGCCCAATGATGCGTGTACA 216
              ||||||||||||||||||||||||||||||||||||
Db       3015 CTTTCCACATCCATGAAGCCCAATGATGCGTGTACA 3050


RESULT 15
AAF98469
ID   AAF98469 standard; cDNA; 3550 BP.
XX
```

AC AAF98469;
XX
DT 07-JUN-2001 (first entry)
XX
DE Human cDNA clone CJ145_1 sequence SEQ ID 160.
XX
KW Human; secreted protein; nutrient; cytokine modulator; proliferation;
KW differentiation; immune system modulator; tissue growth; chemotactic;
KW haemostatic; thrombolytic; anti-inflammatory; tumour inhibition; ss;
KW haematopoiesis.
XX
OS Homo sapiens.
XX
PN WO200119988-A1.
XX
PD 22-MAR-2001.
XX
PF 14-SEP-2000; 2000WO-US25135.
XX
PR 17-SEP-1999; 99US-0398829.
XX
PA (GEMY) GENETICS INST INC.
XX
PI Jacobs K, McCoy JM, LaVallie ER, Collins-Racie LA, Evans C;
PI Merberg D, Treacy M, Bowman MR, Spaulding V, Agostino MJ;
XX
DR WPI; 2001-244801/25.
DR P-PSDB; AAB90731.
XX
PT Isolated nucleic acids encoding polypeptides, useful for modulating
PT e.g. cytokine and cell proliferation/differentiation activity, the
PT immune system and hematopoiesis regulating activity -
XX
PS Disclosure; Page 486-487; 557pp; English.
XX
CC Human cDNA clones represented in AAF98374 - AAF98489 encode secreted
CC proteins AAB90667 - AAB90750. The cDNA clones are isolated from various
CC tissue types, and may be used in the prevention, treatment and diagnosis
CC of diseases associated with inappropriate protein expression. The
CC polypeptides and nucleic acids may be used as nutrients or to modulate
CC cytokine and cell proliferation/differentiation activity and may also be
CC involved in modulation of the immune system. The cDNA sequences,
CC proteins, their agonists and/or antagonists exhibit haematopoiesis
CC regulating activity; tissue growth activity; activin/inhibin activity;
CC chemotactic/chemokinetic activity; haemostatic and thrombolytic
CC activity; receptor/ligand activity; anti-inflammatory activity;
CC haematopoiesis activity; cadherin/tumour suppressor activity; and/or
CC tumour inhibition activity. Included in the invention are probes
CC represented in AAF98490 - AAF98572 which are specific for the cDNA clones
CC encoding the secreted proteins.
XX
SQ Sequence 3550 BP; 957 A; 994 C; 856 G; 742 T; 1 other;

Query Match 100.0%; Score 216; DB 22; Length 3550;
Best Local Similarity 100.0%; Pred. No. 4e-52;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 CCGCCGCCCCGCCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2835 CCGCCGCCCCGCCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC 2894

Qy         61 CAGGCCGTGACTGTCTCGAGGCAGCCCAGCCTCAACGCCTACAACTCACTGACAAGGTCG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2895 CAGGCCGTGACTGTCTCGAGGCAGCCCAGCCTCAACGCCTACAACTCACTGACAAGGTCG 2954

Qy        121 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2955 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCC 3014

Qy        181 CTTTCCACATCCATGAAGCCCAATGATGCGTGTACA 216
              ||||||||||||||||||||||||||||||||||||
Db       3015 CTTTCCACATCCATGAAGCCCAATGATGCGTGTACA 3050
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Job time : 59.8323 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

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Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

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Maximum DB seq length: 2000000000

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
c	1	35.4	16.4	1971	2	US-08-818-253-7	Sequence 7, Appli
c	2	35.4	16.4	1971	3	US-08-818-252-7	Sequence 7, Appli
c	3	35.2	16.3	13987	2	US-08-804-227C-13	Sequence 13, Appl
c	4	35.2	16.3	43280	2	US-08-804-227C-1	Sequence 1, Appli
c	5	34.4	15.9	4403765	3	US-09-103-840A-2	Sequence 2, Appli
c	6	34.4	15.9	4411529	3	US-09-103-840A-1	Sequence 1, Appli
c	7	33.8	15.6	846	4	US-09-252-991A-8905	Sequence 8905, Ap
	8	33.8	15.6	1026	4	US-09-252-991A-1737	Sequence 1737, Ap
	9	33.8	15.6	2667	4	US-09-252-991A-9254	Sequence 9254, Ap
	10	33.8	15.6	3228	4	US-09-252-991A-1816	Sequence 1816, Ap
c	11	33.8	15.6	3546	4	US-09-252-991A-2143	Sequence 2143, Ap
c	12	33.2	15.4	630	4	US-09-252-991A-7012	Sequence 7012, Ap
	13	33.2	15.4	1548	4	US-09-252-991A-7061	Sequence 7061, Ap
	14	33.2	15.4	1581	4	US-09-252-991A-7117	Sequence 7117, Ap
	15	33	15.3	1536	3	US-08-993-359-29	Sequence 29, Appl
	16	33	15.3	1536	4	US-09-482-558A-29	Sequence 29, Appl
	17	32	14.8	1153	2	US-08-869-793-5	Sequence 5, Appli
	18	32	14.8	1162	4	US-09-620-312D-982	Sequence 982, App
	19	31.8	14.7	1119	4	US-09-170-496D-65	Sequence 65, Appl
	20	31.8	14.7	1119	4	US-09-170-496D-199	Sequence 199, App
	21	31.8	14.7	1679	1	US-08-202-056-6	Sequence 6, Appli
	22	31.8	14.7	1679	1	US-08-076-093A-5	Sequence 5, Appli
	23	31.8	14.7	1679	1	US-08-701-265-5	Sequence 5, Appli
	24	31.8	14.7	1679	2	US-08-284-586-5	Sequence 5, Appli
	25	31.8	14.7	1679	2	US-08-805-478-5	Sequence 5, Appli
	26	31.8	14.7	1679	2	US-08-802-627A-5	Sequence 5, Appli
	27	31.8	14.7	1679	2	US-08-801-238-5	Sequence 5, Appli
	28	31.8	14.7	1679	2	US-08-801-228-5	Sequence 5, Appli
	29	31.8	14.7	1679	3	US-09-104-296-5	Sequence 5, Appli
	30	31.8	14.7	1679	5	PCT-US94-06380-3	Sequence 3, Appli
	31	31.8	14.7	2818	3	US-08-982-493-7	Sequence 7, Appli
	32	31.8	14.7	2818	3	US-08-628-655-1	Sequence 1, Appli
c	33	31.6	14.6	882	4	US-09-252-991A-1751	Sequence 1751, Ap
	34	31.6	14.6	1449	4	US-09-252-991A-1976	Sequence 1976, Ap
	35	31.2	14.4	1320	3	US-09-221-654-1	Sequence 1, Appli
	36	31.2	14.4	1320	3	US-08-989-358A-1	Sequence 1, Appli
	37	31.2	14.4	1593	3	US-08-993-359-23	Sequence 23, Appl
	38	31.2	14.4	1593	4	US-09-482-558A-23	Sequence 23, Appl
c	39	31.2	14.4	1932	4	US-09-215-418-3	Sequence 3, Appli
c	40	30.6	14.2	4833	4	US-09-513-783A-21	Sequence 21, Appl
c	41	30.4	14.1	77536	4	US-09-410-551B-1	Sequence 1, Appli
c	42	30.2	14.0	468	4	US-09-252-991A-7286	Sequence 7286, Ap
c	43	30.2	14.0	6462	4	US-09-792-594-10	Sequence 10, Appl
	44	30	13.9	882	4	US-09-252-991A-10864	Sequence 10864, A
c	45	30	13.9	1203	4	US-09-252-991A-10820	Sequence 10820, A

ALIGNMENTS

RESULT 1
US-08-818-253-7/c
; Sequence 7, Application US/08818253
; Patent No. 5998204
; GENERAL INFORMATION:
; APPLICANT: Tsien, Roger Y.
; APPLICANT: Miyawaki, Atsushi
; TITLE OF INVENTION: FLUORESCENT PROTEIN SENSORS FOR
; TITLE OF INVENTION: DETECTION OF ANALYTES
; NUMBER OF SEQUENCES: 61
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: FastSEQ for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/818,253
; FILING DATE: 14-MAR-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Haile, Ph.D., Lisa A.
; REGISTRATION NUMBER: 38,347
; REFERENCE/DOCKET NUMBER: 07257/043001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1971 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 1...1968
US-08-818-253-7

Query Match 16.4%; Score 35.4; DB 2; Length 1971;
Best Local Similarity 61.3%; Pred. No. 0.31;
Matches 57; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

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Qy          2 CGCCGCCCGCCCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGCC 61
              ||||| ||  | ||   ||| ||| | ||| || |||| ||||||||  ||| |    |
Db        112 CGCCGTCCAGCTCGACCAGGATGGGCACCACCCCGGTGAACAGCTCCTCGCCCTTGCTCA 53

Qy         62 AGGCCGTGACTGTCTCGAGGCAGCCCAGCCTCA 94
                | | | | | |   | ||   |||||||  ||
Db         52 CGTCGGCGGCGGCGCCCAGCAGGCCCAGCAGCA 20


RESULT 2
US-08-818-252-7/c
; Sequence 7, Application US/08818252B
; Patent No. 6197928
; GENERAL INFORMATION:
;  APPLICANT: Tsien, Roger Y.
;  APPLICANT: Miyawaki, Atsushi
;  TITLE OF INVENTION: FLUORESCENT PROTEIN SENSORS FOR
;  TITLE OF INVENTION: DETECTION OF ANALYTES
;  FILE REFERENCE: 07257/042001
;  CURRENT APPLICATION NUMBER: US/08/818,252B
;  CURRENT FILING DATE: 1997-03-14
;  NUMBER OF SEQ ID NOS: 56
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7
;   LENGTH: 1971
;   TYPE: DNA
;   ORGANISM: Aequorea victoria
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (0)...(1968)
US-08-818-252-7

  Query Match             16.4%;  Score 35.4;  DB 3;  Length 1971;
  Best Local Similarity   61.3%;  Pred. No. 0.31;
  Matches   57;  Conservative    0;  Mismatches   36;  Indels    0;  Gaps    0;

Qy          2 CGCCGCCCGCCCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGCC 61
              ||||| ||  | ||   ||| ||| | ||| || |||| ||||||||  ||| |    |
Db        112 CGCCGTCCAGCTCGACCAGGATGGGCACCACCCCGGTGAACAGCTCCTCGCCCTTGCTCA 53

Qy         62 AGGCCGTGACTGTCTCGAGGCAGCCCAGCCTCA 94
               | | | | | |   | ||   |||||||  ||
Db         52 CGTCGGCGGCGGCGCCCAGCAGGCCCAGCAGCA 20


RESULT 3
US-08-804-227C-13/c
; Sequence 13, Application US/08804227C
; Patent No. 5876991
;  GENERAL INFORMATION:
;    APPLICANT:  DeHoff, Bradley S.
;    APPLICANT:  Kuhstoss, Stuart A.
;    APPLICANT:  Rosteck, Paul R., Jr.
;    APPLICANT:  Sutton, Kimberly L.
;    TITLE OF INVENTION:  POLYKETIDE SYNTHASE GENES
;    NUMBER OF SEQUENCES:  15
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  THOMAS G. PLANT  1501
;      STREET:  LILLY CORPORATE CENTER
;      CITY:  INDIANAPOLIS
;      STATE:  IN
;      COUNTRY:  USA
;      ZIP:  46285
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  MS-DOS
;      SOFTWARE:  ASCI(DOS) Text only
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/804,227C
;      FILING DATE:  February 21, 1997
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Plant, Thomas, G.
;      REGISTRATION NUMBER:  35,784
;      REFERENCE/DOCKET NUMBER:  X-8231
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  317-276-2459
;  INFORMATION FOR SEQ ID NO:  13:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  13987 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  350..13987
US-08-804-227C-13

  Query Match             16.3%;  Score 35.2;  DB 2;  Length 13987;
  Best Local Similarity   48.5%;  Pred. No. 0.58;
  Matches   97;  Conservative    0;  Mismatches  103;  Indels    0;  Gaps    0;

Qy          2 CGCCGCCCGCCCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGCC 61
              || ||  || |  || | ||  |  |||  ||  |  |  ||| |  |||   ||
Db       1346 CGGCGAGCGGCGTGCTGCGGCCGCTGTCCGCCCCCGCCCCGAGCACGGCGCCCAGTGCGG 1287

Qy         62 AGGCCGTGACTGTCTCGAGGCAGCCCAGCCTCAACGCCTACAACTCACTGACAAGGTCGG 121
               |||  ||| |  |||  |   |      |    | | | || |||   |    || |||
Db       1286 CCGCCTCGACGGGGTCGCCGGCCCGGGTGCCGGTCCCGTGCAGCTCGACGTAGCGGACGG 1227

Qy        122 GGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCCC 181
              || |  ||  |||||| | |    |  || |   | |  || | | ||||  ||  |||
Db       1226 CGCCGGTGCTGACGCCCGCCCGCCGGTAGGCCTGGCGCAGCACAGCTTCCTGCGCCTCCC 1167

Qy        182 TTTCCACATCCATGAAGCCC 201
              ||   |    ||| || |
Db       1166 GGTCGGGAGTGGTGAGGCTC 1147


RESULT 4
US-08-804-227C-1/c
; Sequence 1, Application US/08804227C
; Patent No. 5876991
;  GENERAL INFORMATION:
;    APPLICANT:  DeHoff, Bradley S.
;    APPLICANT:  Kuhstoss, Stuart A.
;    APPLICANT:  Rosteck, Paul R., Jr.
;    APPLICANT:  Sutton, Kimberly L.
;    TITLE OF INVENTION:  POLYKETIDE SYNTHASE GENES
;    NUMBER OF SEQUENCES:  15
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  THOMAS G. PLANT  1501
;      STREET:  LILLY CORPORATE CENTER
;      CITY:  INDIANAPOLIS
;      STATE:  IN
;      COUNTRY:  USA
;      ZIP:  46285
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  MS-DOS
;      SOFTWARE:  ASCI(DOS) Text only
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/804,227C
;      FILING DATE:  February 21, 1997
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Plant, Thomas, G.
;      REGISTRATION NUMBER:  35,784
;      REFERENCE/DOCKET NUMBER:  X-8231
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  317-276-2459
;  INFORMATION FOR SEQ ID NO:  1:
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;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  43280 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  816..14234
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  14351..19945
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  20010..31199
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  31232..36067
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  36249..41774
US-08-804-227C-1

  Query Match             16.3%;  Score 35.2;  DB 2;  Length 43280;
  Best Local Similarity   48.5%;  Pred. No. 0.78;
  Matches   97;  Conservative    0;  Mismatches  103;  Indels    0;  Gaps    0;

Qy          2 CGCCGCCCGCCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGCC 61
              || ||  || |  || | ||  |   |||  ||  |  |  ||| |   |||   ||
Db       1896 CGGCGAGCGGCGTGCTGCGGCCGCTGTCCGCCCCCGCCCCGAGCACGGCGCCCAGTGCGG 1837

Qy         62 AGGCCGTGACTGTCTCGAGGCAGCCCAGCCTCAACGCCTACAACTCACTGACAAGGTCGG 121
                |||  ||| |  |||  |   |      |   | | | || |||   |    || |||
Db       1836 CCGCCTCGACGGGGTCGCCGGCCCGGGTGCCGGTCCCGTGCAGCTCGACGTAGCGGACGG 1777

Qy        122 GGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCCC 181
              || |  ||  |||||| | |    |  || |   | |  || | | |||| ||  |||
Db       1776 CGCCGGTGCTGACGCCCGCCCGCCGGTAGGCCTGGCGCAGCACAGCTTCCTGCGCCTCCC 1717

Qy        182 TTTCCACATCCATGAAGCCC 201
                ||   |    ||| || |
Db       1716 GGTCGGGAGTGGTGAGGCTC 1697


RESULT 5
US-09-103-840A-2/c
; Sequence 2, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
;  APPLICANT: FLEISCHMAN, Robert D.
;  APPLICANT:  WHITE, Owen R.
;  APPLICANT:  FRASER, Claire M.
;  APPLICANT:  VENTER, John C.
;  TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
;  TITLE OF INVENTION:  TUBERCULOSIS
;  FILE REFERENCE: 24366-20007.00
;  CURRENT APPLICATION NUMBER: US/09/103,840A
;  CURRENT FILING DATE:  1998-06-24
;  NUMBER OF SEQ ID NOS: 2
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
;   LENGTH: 4403765
;   TYPE: DNA
;   ORGANISM: Mycobacterium tuberculosis
;   FEATURE:
;   OTHER INFORMATION: CDC 1551
;   OTHER INFORMATION: "n" bases at various positions throughout the sequence
;   OTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2

  Query Match             15.9%;  Score 34.4;  DB 3;  Length 4403765;
  Best Local Similarity   57.4%;  Pred. No. 4.2;
  Matches   62;  Conservative    0;  Mismatches   46;  Indels    0;  Gaps    0;

Qy         22 GTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGCCAGGCCGTGACTGTCTCGAGG 81
              | | | |||    ||  |  ||||||   | |  |  | | ||| | ||    || | ||
Db     745995 GGGTATTCCTCGTAGAGGGCCAGCTCGTTGGCTACCCGGCCGGCGGCGATCAGCTGGCGG 745936

Qy         82 CAGCCCAGCCTCAACGCCTACAACTCACTGACAAGGTCGGGGCTGAAG 129
              | | || ||  || || | |||| | | | || | ||||||  || |
Db     745935 CCGTCCTGCACCAGCGACGACAACGCCCCGCCACGCTCGGGGTCGACG 745888


RESULT 6
US-09-103-840A-1/c
; Sequence 1, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
;  APPLICANT: FLEISCHMAN, Robert D.
;  APPLICANT:  WHITE, Owen R.
;  APPLICANT:  FRASER, Claire M.
;  APPLICANT:  VENTER, John C.
;  TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
;  TITLE OF INVENTION:  TUBERCULOSIS
;  FILE REFERENCE: 24366-20007.00
;  CURRENT APPLICATION NUMBER: US/09/103,840A
;  CURRENT FILING DATE:  1998-06-24
;  NUMBER OF SEQ ID NOS: 2
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
;   LENGTH: 4411529
;   TYPE: DNA
;   ORGANISM: Mycobacterium tuberculosis
;   OTHER INFORMATION: H37Rv
US-09-103-840A-1

  Query Match             15.9%;  Score 34.4;  DB 3;  Length 4411529;
  Best Local Similarity   57.4%;  Pred. No. 4.2;
  Matches   62;  Conservative    0;  Mismatches   46;  Indels    0;  Gaps    0;

Qy         22 GTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGCCAGGCCGTGACTGTCTCGAGG 81
              | | | |||    ||  |  ||||||   | |  |  | | ||| | ||    || | ||
Db     744035 GGGTATTCCTCGTAGAGGGCCAGCTCGTTGGCTACCCGGCCGGCGGCGATCAGCTGGCGG 743976

Qy         82 CAGCCCAGCCTCAACGCCTACAACTCACTGACAAGGTCGGGGCTGAAG 129
              | | || ||  || || | |||| | | | || | ||||||  || |
Db     743975 CCGTCCTGCACCAGCGACGACAACGCCCCGCCACGCTCGGGGTCGACG 743928


RESULT 7
US-09-252-991A-8905/c
; Sequence 8905, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
;  APPLICANT:  Marc J. Rubenfield et al.
;  TITLE OF INVENTION:  NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONA
;  TITLE OF INVENTION:  AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE:  107196.136
;  CURRENT APPLICATION NUMBER: US/09/252,991A
;  CURRENT FILING DATE:  1999-02-18
;  PRIOR APPLICATION NUMBER:  US 60/074,788
;  PRIOR FILING DATE:  1998-02-18
;  PRIOR APPLICATION NUMBER:  US 60/094,190
;  PRIOR FILING DATE:  1998-07-27
;  NUMBER OF SEQ ID NOS:  33142
; SEQ ID NO 8905
;   LENGTH: 846
;   TYPE: DNA
;   ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-8905

  Query Match             15.6%;  Score 33.8;  DB 4;  Length 846;
  Best Local Similarity   49.2%;  Pred. No. 0.72;
  Matches   89;  Conservative    0;  Mismatches   92;  Indels    0;  Gaps    0;

Qy          2 CGCCGCCCGCCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGCC 61
```

```
Db        343 CGTGGCAGCGCGAGCACATCTTCTGCGCCATCGCCTTGCCGCGCGCCAGGTCGGCGGGCG 284

Qy         62 AGGCCGTGACTGTCTCGAGGCAGCCCAGCCTCAACGCCTACAACTCACTGACAAGGTCGG 121

Db        283 CGTCCGGGCCCGGCACGGCGGCGGCCAGCGGCAGGGAAAGCAGGGCCGAGAGGCAGCCGG 224

Qy        122 GGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCCC 181

Db        223 CCAGCCAGCGTTTACGCTCAGTCATGCTGCCAGGGCCCCCGCAGCCAGCCGTGGATGTCG 164

Qy        182 T 182

Db        163 T 163
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RESULT 8
US-09-252-991A-1737
; Sequence 1737, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 1737
; LENGTH: 1026
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-1737

Query Match 15.6%; Score 33.8; DB 4; Length 1026;
Best Local Similarity 54.4%; Pred. No. 0.76;
Matches 68; Conservative 0; Mismatches 57; Indels 0; Gaps 0;

```
Qy         62 AGGCCGTGACTGTCTCGAGGCAGCCCAGCCTCAACGCCTACAACTCACTGACAAGGTCGG 121

Db        271 AGGCCGGATCAACATCAAGGAAGTCCTGAGCGAAGGCCAGGAAGTCATCGTCCAGGTCGA 330

Qy        122 GGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCCC 181

Db        331 GAAGGAAGAGCGCGGCAACAAGGGCGCCGCCCTGACCACCTTCATCAGCCTGGCCGGCCG 390

Qy        182 TTTCC 186

Db        391 TTACC 395
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RESULT 9
US-09-252-991A-9254
; Sequence 9254, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 9254
; LENGTH: 2667
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-9254

Query Match 15.6%; Score 33.8; DB 4; Length 2667;
Best Local Similarity 49.2%; Pred. No. 0.96;
Matches 89; Conservative 0; Mismatches 92; Indels 0; Gaps 0;

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Qy          2 CGCCGCCCGCCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGCC 61

Db         38 CGTGGCAGCGCGAGCACATCTTCTGCGCCATCGCCTTGCCGCGCGCCAGGTCGGCGGGCG 97

Qy         62 AGGCCGTGACTGTCTCGAGGCAGCCCAGCCTCAACGCCTACAACTCACTGACAAGGTCGG 121

Db         98 CGTCCGGGCCCGGCACGGCGGCGGCCAGCGGCAGGGAAAGCAGGGCCGAGAGGCAGCCGG 157

Qy        122 GGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCCC 181

Db        158 CCAGCCAGCGTTTACGCTCAGTCATGCTGCCAGGGCCCCCGCAGCCAGCCGTGGATGTCG 217

Qy        182 T 182

Db        218 T 218
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RESULT 10
US-09-252-991A-1816
; Sequence 1816, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONA
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 1816
; LENGTH: 3228
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-1816

Query Match 15.6%; Score 33.8; DB 4; Length 3228;
Best Local Similarity 54.4%; Pred. No. 1;
Matches 68; Conservative 0; Mismatches 57; Indels 0; Gaps 0;

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Qy         62 AGGCCGTGACTGTCTCGAGGCAGCCCAGCCTCAACGCCTACAACTCACTGACAAGGTCGG 121

Db        303 AGGCCGGATCAACATCAAGGAAGTCCTGAGCGAAGGCCAGGAAGTCATCGTCCAGGTCGA 362

Qy        122 GGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCCC 181

Db        363 GAAGGAAGAGCGCGGCAACAAGGGCGCCGCCCTGACCACCTTCATCAGCCTGGCCGGCCG 422

Qy        182 TTTCC 186

Db        423 TTACC 427
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RESULT 11
US-09-252-991A-2143/c
; Sequence 2143, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONA
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136

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;  CURRENT APPLICATION NUMBER: US/09/252,991A
;  CURRENT FILING DATE:  1999-02-18
;  PRIOR APPLICATION NUMBER:  US 60/074,788
;  PRIOR FILING DATE:  1998-02-18
;  PRIOR APPLICATION NUMBER:  US 60/094,190
;  PRIOR FILING DATE:  1998-07-27
;  NUMBER OF SEQ ID NOS:  33142
; SEQ ID NO 2143
;   LENGTH: 3546
;   TYPE: DNA
;   ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-2143

  Query Match            15.6%;  Score 33.8;  DB 4;  Length 3546;
  Best Local Similarity  54.4%;  Pred. No. 1;
  Matches   68;  Conservative    0;  Mismatches   57;  Indels    0;  Gaps    0;

Qy         62 AGGCCGTGACTGTCTCGAGGCAGCCCAGCCTCAACGCCTACAACTCACTGACAAGGTCGG 121
              ||||||   |    || ||| || || |    || |||   || |||  | | ||||||
Db       3064 AGGCCGGATCAACATCAAGGAAGTCCTGAGCGAAGGCCAGGAAGTCATCGTCCAGGTCGA 3005

Qy        122 GGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCCC 181
              |   |||| |  || |  |      |||| |  ||| ||   | || |||   |  ||
Db       3004 GAAGGAAGAGCGCGGCAACAAGGGCGCCGCCCTGACCACCTTCATCAGCCTGGCCGGCCG 2945

Qy        182 TTTCC 186
              || ||
Db       2944 TTACC 2940


RESULT 12
US-09-252-991A-7012/c
; Sequence 7012, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
;  APPLICANT:  Marc J. Rubenfield et al.
;  TITLE OF INVENTION:  NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
;  TITLE OF INVENTION:  AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE:  107196.136
;  CURRENT APPLICATION NUMBER: US/09/252,991A
;  CURRENT FILING DATE:  1999-02-18
;  PRIOR APPLICATION NUMBER:  US 60/074,788
;  PRIOR FILING DATE:  1998-02-18
;  PRIOR APPLICATION NUMBER:  US 60/094,190
;  PRIOR FILING DATE:  1998-07-27
;  NUMBER OF SEQ ID NOS:  33142
; SEQ ID NO 7012
;   LENGTH: 630
;   TYPE: DNA
;   ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-7012

  Query Match            15.4%;  Score 33.2;  DB 4;  Length 630;
  Best Local Similarity  53.0%;  Pred. No. 0.99;
  Matches   71;  Conservative    0;  Mismatches   63;  Indels    0;  Gaps    0;

Qy          7 CCCGCCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGCCAGGCC 66
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Qy        127 AAGCGTACGCCCTC 140
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Db         83 AGGCAGTCGCCCTC 70


RESULT 13
US-09-252-991A-7061
; Sequence 7061, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
;  APPLICANT:  Marc J. Rubenfield et al.
;  TITLE OF INVENTION:  NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONA
;  TITLE OF INVENTION:  AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE:  107196.136
;  CURRENT APPLICATION NUMBER: US/09/252,991A
;  CURRENT FILING DATE:  1999-02-18
;  PRIOR APPLICATION NUMBER:  US 60/074,788
;  PRIOR FILING DATE:  1998-02-18
;  PRIOR APPLICATION NUMBER:  US 60/094,190
;  PRIOR FILING DATE:  1998-07-27
;  NUMBER OF SEQ ID NOS:  33142
; SEQ ID NO 7061
;   LENGTH: 1548
;   TYPE: DNA
;   ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-7061

  Query Match            15.4%;  Score 33.2;  DB 4;  Length 1548;
  Best Local Similarity  53.0%;  Pred. No. 1.2;
  Matches   71;  Conservative    0;  Mismatches   63;  Indels    0;  Gaps    0;

Qy          7 CCCGCCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGCCAGGCC 66
              || ||| ||||  | |  |  | |  | |    | |   |||| |||  |||||| |||
Db        532 CCTGCCGCGCATCGAGGTGGATGCGGCGATCGCCGCCCGTCCCGGCCGGCTGGCCTGGCG 591

Qy         67 GTGACTGTCTCGAGGCAGCCCAGCCTCAACGCCTACAACTCACTGACAAGGTCGGGGCTG 126
                    | ||| | |||||    ||  || | || | |  |  |||||  | |
Db        592 CATCTATCGTGGAGCCCGCCCATGAGCATGGCTTCCAGCCCGTTCCCAAGGAGGCGCGAC 651

Qy        127 AAGCGTACGCCCTC 140
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Db        652 AGGCAGTCGCCCTC 665


RESULT 14
US-09-252-991A-7117
; Sequence 7117, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
;  APPLICANT:  Marc J. Rubenfield et al.
;  TITLE OF INVENTION:  NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONA
;  TITLE OF INVENTION:  AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE:  107196.136
;  CURRENT APPLICATION NUMBER: US/09/252,991A
;  CURRENT FILING DATE:  1999-02-18
;  PRIOR APPLICATION NUMBER:  US 60/074,788
;  PRIOR FILING DATE:  1998-02-18
;  PRIOR APPLICATION NUMBER:  US 60/094,190
;  PRIOR FILING DATE:  1998-07-27
;  NUMBER OF SEQ ID NOS:  33142
; SEQ ID NO 7117
;   LENGTH: 1581
;   TYPE: DNA
;   ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-7117

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  Best Local Similarity  53.0%;  Pred. No. 1.3;
  Matches   71;  Conservative    0;  Mismatches   63;  Indels    0;  Gaps    0;

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              || ||| ||||  | |  |  | |  | |    | |   |||| |||  |||||| |||
Db        623 CCTGCCGCGCATCGAGGTGGATGCGGCGATCGCCGCCCGTCCCGGCCGGCTGGCCTGGCG 682

Qy         67 GTGACTGTCTCGAGGCAGCCCAGCCTCAACGCCTACAACTCACTGACAAGGTCGGGGCTG 126
                    | ||| | |||||    ||  || | || | |  |  |||||  | |
Db        683 CATCTATCGTGGAGCCCGCCCATGAGCATGGCTTCCAGCCCGTTCCCAAGGAGGCGCGAC 742

Qy        127 AAGCGTACGCCCTC 140
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Db        743 AGGCAGTCGCCCTC 756
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RESULT 15
US-08-993-359-29
; Sequence 29, Application US/08993359A
; Patent No. 6039942
; GENERAL INFORMATION:
;  APPLICANT: Lassen, Soren F.
;  APPLICANT: Bech, Lisbeth
;  APPLICANT: Ohmann, Anders
;  APPLICANT: Breinholt, Jens
;  APPLICANT: Fuglsang, Claus C.
;  APPLICANT: Ostergaard, Peter R.
;  TITLE OF INVENTION: Phytase Polypeptides
;  FILE REFERENCE: 5383.500-US
;  CURRENT APPLICATION NUMBER: US/08/993,359A
;  CURRENT FILING DATE: 1997-12-18
;  EARLIER APPLICATION NUMBER: 1480/96
;  EARLIER FILING DATE: 1996-12-20
;  EARLIER APPLICATION NUMBER: 1481/96
;  EARLIER FILING DATE: 1996-12-20
;  EARLIER APPLICATION NUMBER: 0301/97
;  EARLIER FILING DATE: 1997-03-18
;  EARLIER APPLICATION NUMBER: 0529/97
;  EARLIER FILING DATE: 1997-05-07
;  EARLIER APPLICATION NUMBER: 1388/97
;  EARLIER FILING DATE: 1997-12-01
;  EARLIER APPLICATION NUMBER: 60/046,082
;  EARLIER FILING DATE: 1997-05-09
;  NUMBER OF SEQ ID NOS: 32
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 29
;   LENGTH: 1536
;   TYPE: DNA
;   ORGANISM: Trametes pubescens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (79)...(1407)
;   NAME/KEY: mat_peptide
;   LOCATION: (130)...(1407)
;   NAME/KEY: sig_peptide
;   LOCATION: (79)...(129)
US-08-993-359-29

  Query Match            15.3%;  Score 33;  DB 3;  Length 1536;
  Best Local Similarity  53.5%;  Pred. No. 1.4;
  Matches   69;  Conservative    0;  Mismatches   60;  Indels    0;  Gaps    0;

Qy         11 CCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGCCAGGCCGTGA 70
              ||  |||  | || |  | |||| | | || || | | |  |   | |  |||  ||||
Db        950 CCGTGCAAGGCGTCGGGTACATCAACGAGCTCATCGCGCGCCTCACCGCGCAGAACGTGT 1009

Qy         71 CTGTCTCGAGGCAGCCCAGCCTCAACGCCTACAACTCACTGACAAGGTCGGGGCTGAAGC 130
                | | |   | |||| | | |  ||    | ||  ||| |     | ||    ||| || |
Db       1010 CCGACCACACGCAGACGAACAGCACACTCGACTCCTCGCCCGAGACGTTCCCGCTCAACC 1069

Qy        131 GTACGCCCT 139
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Db       1070 GCACGCTCT 1078


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Job time : 27.4914 secs
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: September 30, 2003, 16:44:06 ; Search time 53.2004 Seconds
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Title: US-09-856-681-3
Perfect score: 216
Sequence: 1 ccgccgcccgccccgcagag.....agcccaatgatgcgtgtaca 216

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1678620 seqs, 1244745471 residues

Total number of hits satisfying chosen parameters: 3357240

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
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	2	216	100.0	1472	11	US-09-925-299-60	Sequence 60, Appl
	3	216	100.0	3333	11	US-09-991-053-5	Sequence 5, Appli
	4	216	100.0	3333	11	US-09-957-187-5	Sequence 5, Appli
	5	216	100.0	3498	11	US-09-991-053-3	Sequence 3, Appli
	6	216	100.0	3498	11	US-09-957-187-3	Sequence 3, Appli
	7	216	100.0	4250	11	US-09-957-187-84	Sequence 84, Appl
c	8	168	77.8	460	11	US-09-918-995-3799	Sequence 3799, Ap
	9	55	25.5	6767	11	US-09-764-891-6944	Sequence 6944, Ap
	10	55	25.5	6773	11	US-09-764-891-6943	Sequence 6943, Ap
	11	53.4	24.7	662	11	US-09-764-891-810	Sequence 810, App
c	12	37.4	17.3	765	13	US-10-027-632-166826	Sequence 166826,
c	13	35.4	16.4	1971	10	US-09-554-000-7	Sequence 7, Appli
	14	35.2	16.3	936	14	US-10-128-714-2578	Sequence 2578, Ap
	15	35.2	16.3	936	14	US-10-128-714-7578	Sequence 7578, Ap
	16	35.2	16.3	1015	14	US-10-128-714-1578	Sequence 1578, Ap
	17	35.2	16.3	1015	14	US-10-128-714-6578	Sequence 6578, Ap
	18	35.2	16.3	3015	14	US-10-128-714-578	Sequence 578, App
	19	35.2	16.3	3015	14	US-10-128-714-5578	Sequence 5578, Ap
	20	33.6	15.6	3970	14	US-10-158-646-9	Sequence 9, Appli
c	21	33.2	15.4	936	14	US-10-187-267A-34	Sequence 34, Appl
	22	33.2	15.4	1458	14	US-10-156-761-6684	Sequence 6684, Ap
c	23	33.2	15.4	36321	14	US-10-187-267A-1	Sequence 1, Appli
	24	33.2	15.4	9025608	14	US-10-156-761-1	Sequence 1, Appli
c	25	32.8	15.2	1131	14	US-10-156-761-1908	Sequence 1908, Ap
c	26	32.8	15.2	9025608	14	US-10-156-761-1	Sequence 1, Appli
	27	32.4	15.0	1167	14	US-10-156-761-541	Sequence 541, App
	28	32	14.8	519	9	US-09-864-761-22739	Sequence 22739, A
	29	32	14.8	1095	12	US-09-109-203A-4	Sequence 4, Appli
	30	32	14.8	1162	14	US-10-037-270-982	Sequence 982, App
	31	32	14.8	1172	12	US-10-199-672-209	Sequence 209, App
	32	32	14.8	1172	12	US-10-187-749-209	Sequence 209, App
	33	32	14.8	1172	12	US-10-194-457-209	Sequence 209, App
	34	32	14.8	1172	12	US-10-184-642-209	Sequence 209, App
	35	32	14.8	1172	12	US-10-196-747-209	Sequence 209, App
	36	32	14.8	1172	12	US-10-173-689-209	Sequence 209, App
	37	32	14.8	1172	12	US-10-173-690-209	Sequence 209, App
	38	32	14.8	1172	12	US-10-173-691-209	Sequence 209, App
	39	32	14.8	1172	12	US-10-173-692-209	Sequence 209, App
	40	32	14.8	1172	12	US-10-173-694-209	Sequence 209, App
	41	32	14.8	1172	12	US-10-173-698-209	Sequence 209, App
	42	32	14.8	1172	12	US-10-173-699-209	Sequence 209, App
	43	32	14.8	1172	12	US-10-173-707-209	Sequence 209, App
	44	32	14.8	1172	12	US-10-174-569-209	Sequence 209, App
	45	32	14.8	1172	12	US-10-174-583-209	Sequence 209, App

ALIGNMENTS

RESULT 1
US-09-925-299-60
; Sequence 60, Application US/09925299
; Patent No. US20020055627A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA102
; CURRENT APPLICATION NUMBER: US/09/925,299
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05883
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1556
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 60
; LENGTH: 1472
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (129)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (130)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-925-299-60

Query Match 100.0%; Score 216; DB 9; Length 1472;
Best Local Similarity 100.0%; Pred. No. 5.1e-58;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 CCGCCGCCCGCCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        372 CCGCCGCCCGCCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC 431

Qy         61 CAGGCCGTGACTGTCTCGAGGCAGCCCAGCCTCAACGCCTACAACTCACTGACAAGGTCG 120
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Db        432 CAGGCCGTGACTGTCTCGAGGCAGCCCAGCCTCAACGCCTACAACTCACTGACAAGGTCG 491

Qy        121 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCC 180
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Db        492 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCC 551

Qy        181 CTTTCCACATCCATGAAGCCCAATGATGCGTGTACA 216
              ||||||||||||||||||||||||||||||||||||
Db        552 CTTTCCACATCCATGAAGCCCAATGATGCGTGTACA 587


RESULT 2
US-09-925-299-60
; Sequence 60, Application US/09925299
; Publication No. US20030040617A9
; GENERAL INFORMATION:
;  APPLICANT: Rosen et al.
;  TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
;  FILE REFERENCE: PA102
;  CURRENT APPLICATION NUMBER: US/09/925,299
;  CURRENT FILING DATE:  2001-08-10
;  PRIOR APPLICATION NUMBER: PCT/US00/05883
;  PRIOR FILING DATE: 2000-03-08
;  PRIOR APPLICATION NUMBER: 60/124,270
;  PRIOR FILING DATE: 1999-03-12
;  NUMBER OF SEQ ID NOS: 1556
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 60
;   LENGTH: 1472
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (129)
;   OTHER INFORMATION: n equals a,t,g, or c
;   NAME/KEY: misc_feature
;   LOCATION: (130)
;   OTHER INFORMATION: n equals a,t,g, or c
US-09-925-299-60

  Query Match             100.0%;  Score 216;  DB 11;  Length 1472;
  Best Local Similarity   100.0%;  Pred. No. 5.1e-58;
  Matches  216;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CCGCCGCCCCGCCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        372 CCGCCGCCCCGCCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC 431

Qy         61 CAGGCCGTGACTGTCTCGAGGCAGCCCAGCCTCAACGCCTACAACTCACTGACAAGGTCG 120
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Qy        181 CTTTCCACATCCATGAAGCCCAATGATGCGTGTACA 216
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RESULT 3
US-09-991-053-5
; Sequence 5, Application US/09991053
; Publication No. US20030003532A1
; GENERAL INFORMATION:
;  APPLICANT: Shimkets, Richard A.
;  TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES ENCODING HUMAN SLIT-,
;  TITLE OF INVENTION:  MEGF-, AND ROUNDABOUT-LIKE POLYPEPTIDES
;  FILE REFERENCE: 15966-540 CON S-10
;  CURRENT APPLICATION NUMBER: US/09/991,053
;  CURRENT FILING DATE:  2002-05-23
;  PRIOR APPLICATION NUMBER: USSN 60/123,667
;  PRIOR FILING DATE: 1999-03-09
;  PRIOR APPLICATION NUMBER: 09/520,781
;  PRIOR FILING DATE: 2000-03-08
;  NUMBER OF SEQ ID NOS: 81
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
;   LENGTH: 3333
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (214)..(2865)
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (2882)
;   OTHER INFORMATION: an n may be any one of a or t or g or c
US-09-991-053-5

  Query Match             100.0%;  Score 216;  DB 11;  Length 3333;
  Best Local Similarity   100.0%;  Pred. No. 5.5e-58;
  Matches  216;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CCGCCGCCCCGCCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2925 CCGCCGCCCCGCCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC 2984

Qy         61 CAGGCCGTGACTGTCTCGAGGCAGCCCAGCCTCAACGCCTACAACTCACTGACAAGGTCG 120
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Db       2985 CAGGCCGTGACTGTCTCGAGGCAGCCCAGCCTCAACGCCTACAACTCACTGACAAGGTCG 3044

Qy        121 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCC 180
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Db       3045 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCC 3104

Qy        181 CTTTCCACATCCATGAAGCCCAATGATGCGTGTACA 216
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Db       3105 CTTTCCACATCCATGAAGCCCAATGATGCGTGTACA 3140


RESULT 4
US-09-957-187-5
; Sequence 5, Application US/09957187
; Publication No. US20030054514A1
; GENERAL INFORMATION:
;  APPLICANT: Shimkets, Richard A.
;  APPLICANT:  LaRochelle, William
;  TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES AND PROTEINS ENCODED THEREBY
;  FILE REFERENCE: 15966-540 CIP
;  CURRENT APPLICATION NUMBER: US/09/957,187
;  CURRENT FILING DATE:  2000-09-19
;  PRIOR APPLICATION NUMBER: 60/123,667
;  PRIOR FILING DATE: 1999-03-09
;  PRIOR APPLICATION NUMBER: 09/520,781
;  PRIOR FILING DATE: 2000-03-03
;  PRIOR APPLICATION NUMBER: 60/234,082
;  PRIOR FILING DATE: 2000-09-20
;  PRIOR APPLICATION NUMBER: 60/233,798
;  PRIOR FILING DATE: 2000-09-19
;  PRIOR APPLICATION NUMBER: 60/174,485
;  PRIOR FILING DATE: 2000-01-04
;  NUMBER OF SEQ ID NOS: 85
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; SEQ ID NO 5
;   LENGTH: 3333
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (214)..(2865)
;   NAME/KEY: misc_feature
;   LOCATION: (2882)
;   OTHER INFORMATION: an n may be any one of a or t or g or c
US-09-957-187-5
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  Query Match             100.0%;  Score 216;  DB 11;  Length 3333;
  Best Local Similarity   100.0%;  Pred. No. 5.5e-58;
  Matches  216;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CCGCCGCCCGCCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC 60
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Db       2925 CCGCCGCCCGCCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC 2984

Qy         61 CAGGCCGTGACTGTCTCGAGGCAGCCCAGCCTCAACGCCTACAACTCACTGACAAGGTCG 120
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Db       2985 CAGGCCGTGACTGTCTCGAGGCAGCCCAGCCTCAACGCCTACAACTCACTGACAAGGTCG 3044

Qy        121 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3045 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCC 3104

Qy        181 CTTTCCACATCCATGAAGCCCAATGATGCGTGTACA 216
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Db       3105 CTTTCCACATCCATGAAGCCCAATGATGCGTGTACA 3140


RESULT 5
US-09-991-053-3
; Sequence 3, Application US/09991053
; Publication No. US20030003532A1
; GENERAL INFORMATION:
;  APPLICANT: Shimkets, Richard A.
;  TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES ENCODING HUMAN SLIT-,
;  TITLE OF INVENTION:  MEGF-, AND ROUNDABOUT-LIKE POLYPEPTIDES
;  FILE REFERENCE: 15966-540 CON S-10
;  CURRENT APPLICATION NUMBER: US/09/991,053
;  CURRENT FILING DATE:  2002-05-23
;  PRIOR APPLICATION NUMBER: USSN 60/123,667
;  PRIOR FILING DATE: 1999-03-09
;  PRIOR APPLICATION NUMBER: 09/520,781
;  PRIOR FILING DATE: 2000-03-08
;  NUMBER OF SEQ ID NOS: 81
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
;   LENGTH: 3498
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (214)..(3030)
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (3047)
;   OTHER INFORMATION: an n may be any one of a or t or g or c
US-09-991-053-3

  Query Match             100.0%;  Score 216;  DB 11;  Length 3498;
  Best Local Similarity   100.0%;  Pred. No. 5.5e-58;
  Matches  216;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CCGCCGCCCGCCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3090 CCGCCGCCCGCCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC 3149

Qy         61 CAGGCCGTGACTGTCTCGAGGCAGCCCAGCCTCAACGCCTACAACTCACTGACAAGGTCG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3150 CAGGCCGTGACTGTCTCGAGGCAGCCCAGCCTCAACGCCTACAACTCACTGACAAGGTCG 3209

Qy        121 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3210 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCC 3269

Qy        181 CTTTCCACATCCATGAAGCCCAATGATGCGTGTACA 216
              ||||||||||||||||||||||||||||||||||||
Db       3270 CTTTCCACATCCATGAAGCCCAATGATGCGTGTACA 3305


RESULT 6
US-09-957-187-3
; Sequence 3, Application US/09957187
; Publication No. US20030054514A1
; GENERAL INFORMATION:
;  APPLICANT: Shimkets, Richard A.
;  APPLICANT:  LaRochelle, William
;  TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES AND PROTEINS ENCODED THEREBY
;  FILE REFERENCE: 15966-540 CIP
;  CURRENT APPLICATION NUMBER: US/09/957,187
;  CURRENT FILING DATE:  2000-09-19
;  PRIOR APPLICATION NUMBER: 60/123,667
;  PRIOR FILING DATE: 1999-03-09
;  PRIOR APPLICATION NUMBER: 09/520,781
;  PRIOR FILING DATE: 2000-03-03
;  PRIOR APPLICATION NUMBER: 60/234,082
;  PRIOR FILING DATE: 2000-09-20
;  PRIOR APPLICATION NUMBER: 60/233,798
;  PRIOR FILING DATE: 2000-09-19
;  PRIOR APPLICATION NUMBER: 60/174,485
;  PRIOR FILING DATE: 2000-01-04
;  NUMBER OF SEQ ID NOS: 85
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
;   LENGTH: 3498
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (214)..(3030)
;   NAME/KEY: misc_feature
;   LOCATION: (3047)
;   OTHER INFORMATION: an n may be any one of a or t or g or c
US-09-957-187-3

  Query Match             100.0%;  Score 216;  DB 11;  Length 3498;
  Best Local Similarity   100.0%;  Pred. No. 5.5e-58;
  Matches  216;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CCGCCGCCCGCCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3090 CCGCCGCCCGCCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC 3149

Qy         61 CAGGCCGTGACTGTCTCGAGGCAGCCCAGCCTCAACGCCTACAACTCACTGACAAGGTCG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3150 CAGGCCGTGACTGTCTCGAGGCAGCCCAGCCTCAACGCCTACAACTCACTGACAAGGTCG 3209

Qy        121 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3210 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCC 3269

Qy        181 CTTTCCACATCCATGAAGCCCAATGATGCGTGTACA 216
              ||||||||||||||||||||||||||||||||||||
Db       3270 CTTTCCACATCCATGAAGCCCAATGATGCGTGTACA 3305


RESULT 7
US-09-957-187-84
; Sequence 84, Application US/09957187
; Publication No. US20030054514A1
; GENERAL INFORMATION:
;  APPLICANT: Shimkets, Richard A.
;  APPLICANT:  LaRochelle, William
;  TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES AND PROTEINS ENCODED THEREBY
;  FILE REFERENCE: 15966-540 CIP
;  CURRENT APPLICATION NUMBER: US/09/957,187
;  CURRENT FILING DATE:  2000-09-19
;  PRIOR APPLICATION NUMBER: 60/123,667
;  PRIOR FILING DATE: 1999-03-09
;  PRIOR APPLICATION NUMBER: 09/520,781
;  PRIOR FILING DATE: 2000-03-03
;  PRIOR APPLICATION NUMBER: 60/234,082
;  PRIOR FILING DATE: 2000-09-20
```

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;  PRIOR APPLICATION NUMBER: 60/233,798
;  PRIOR FILING DATE: 2000-09-19
;  PRIOR APPLICATION NUMBER: 60/174,485
;  PRIOR FILING DATE: 2000-01-04
;  NUMBER OF SEQ ID NOS: 85
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 84
;   LENGTH: 4250
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (250)..(3390)
US-09-957-187-84

  Query Match           100.0%;  Score 216;  DB 11;  Length 4250;
  Best Local Similarity  100.0%;  Pred. No. 5.7e-58;
  Matches  216;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CCGCCGCCCGCCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3175 CCGCCGCCCGCCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGC 3234

Qy         61 CAGGCCGTGACTGTCTCGAGGCAGCCCAGCCTCAACGCCTACAACTCACTGACAAGGTCG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3235 CAGGCCGTGACTGTCTCGAGGCAGCCCAGCCTCAACGCCTACAACTCACTGACAAGGTCG 3294

Qy        121 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3295 GGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCC 3354

Qy        181 CTTTCCACATCCATGAAGCCCAATGATGCGTGTACA 216
              ||||||||||||||||||||||||||||||||||||
Db       3355 CTTTCCACATCCATGAAGCCCAATGATGCGTGTACA 3390


RESULT 8
US-09-918-995-3799/c
; Sequence 3799, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
;  APPLICANT: Hyseq, Inc.
;  TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
;  TITLE OF INVENTION:  FROM VARIOUS cDNA LIBRARIES
;  FILE REFERENCE: 20411-756
;  CURRENT APPLICATION NUMBER: US/09/918,995
;  CURRENT FILING DATE:  2001-07-30
;  PRIOR APPLICATION NUMBER: US/09/235,076
;  PRIOR FILING DATE: 1999-01-20
;  NUMBER OF SEQ ID NOS: 38054
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 3799
;   LENGTH: 460
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(460)
;   OTHER INFORMATION: n = A,T,C or G
US-09-918-995-3799

  Query Match           77.8%;  Score 168;  DB 11;  Length 460;
  Best Local Similarity  99.4%;  Pred. No. 4.7e-43;
  Matches  168;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         48 CCAGCCATCTGGCCAGGCCGTGACTGTCTCGAGGCAGCCCAGCCTCAACGCCTACAACTC 107
              |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db        459 CCAGCCATCTGGCCAGNCCGTGACTGTCTCGAGGCAGCCCAGCCTCAACGCCTACAACTC 400

Qy        108 ACTGACAAGGTCGGGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACC 167
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        399 ACTGACAAGGTCGGGGCTGAAGCGTACGCCCTCGCTAAAGCCGGACGTACCCCCCAAACC 340

Qy        168 ATCCTTTGCTCCCCTTTCCACATCCATGAAGCCCAATGATGCGTGTACA 216
              ||||||||||||||||||||||||||||||||||||||||||||||||
Db        339 ATCCTTTGCTCCCCTTTCCACATCCATGAAGCCCAATGATGCGTGTACA 291


RESULT 9
US-09-764-891-6944
; Sequence 6944, Application US/09764891
; Publication No. US20030077808A1
; GENERAL INFORMATION:
;  APPLICANT: Rosen et al.
;  TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
;  FILE REFERENCE: PC006
;  CURRENT APPLICATION NUMBER: US/09/764,891
;  CURRENT FILING DATE:  2001-01-17
;  Prior application data removed - consult PALM or file wrapper
;  NUMBER OF SEQ ID NOS: 10231
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6944
;   LENGTH: 6767
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-764-891-6944

  Query Match           25.5%;  Score 55;  DB 11;  Length 6767;
  Best Local Similarity  64.6%;  Pred. No. 1.4e-07;
  Matches   82;  Conservative    0;  Mismatches   45;  Indels    0;  Gaps    0;

Qy         74 TCTCGAGGCAGCCCAGCCTCAACGCCTACAACTCACTGACAAGGTCGGGGCTGAAGCGTA 133
              |||| || |||  |||| || |    |   | | ||  | ||| |||| || ||| | |
Db       5521 TCTCCAGACAGAGCAGCTACACCAGTAATGGCACTCTTCCTAGGACGGGACTAAAGAGGA 5580

Qy        134 CGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCCCTTTCCACATCCA 193
              |||| ||  |||| || ||||| || || || || ||||||| ||| |   || ||||
Db       5581 CGCCGTCCTTAAAACCTGACGTGCCACCAAAGCCTTCCTTTGTTCCTCAAACCCCATCTG 5640

Qy        194 TGAAGCC 200
              | |  ||
Db       5641 TCAGACC 5647


RESULT 10
US-09-764-891-6943
; Sequence 6943, Application US/09764891
; Publication No. US20030077808A1
; GENERAL INFORMATION:
;  APPLICANT: Rosen et al.
;  TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
;  FILE REFERENCE: PC006
;  CURRENT APPLICATION NUMBER: US/09/764,891
;  CURRENT FILING DATE:  2001-01-17
;  Prior application data removed - consult PALM or file wrapper
;  NUMBER OF SEQ ID NOS: 10231
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6943
;   LENGTH: 6773
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-764-891-6943

  Query Match           25.5%;  Score 55;  DB 11;  Length 6773;
  Best Local Similarity  64.6%;  Pred. No. 1.4e-07;
  Matches   82;  Conservative    0;  Mismatches   45;  Indels    0;  Gaps    0;

Qy         74 TCTCGAGGCAGCCCAGCCTCAACGCCTACAACTCACTGACAAGGTCGGGGCTGAAGCGTA 133
              |||| || |||  |||| || |    |   | | ||  | ||| |||| || ||| | |
Db       5527 TCTCCAGACAGAGCAGCTACACCAGTAATGGCACTCTTCCTAGGACGGGACTAAAGAGGA 5586

Qy        134 CGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCCCTTTCCACATCCA 193
              |||| ||  |||| || ||||| || || || || ||||||| ||| |   || ||||
Db       5587 CGCCGTCCTTAAAACCTGACGTGCCACCAAAGCCTTCCTTTGTTCCTCAAACCCCATCTG 5646

Qy        194 TGAAGCC 200
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                | |  ||
Db       5647 TCAGACC 5653


RESULT 11
US-09-764-891-810
; Sequence 810, Application US/09764891
; Publication No. US20030077808A1
; GENERAL INFORMATION:
;  APPLICANT: Rosen et al.
;  TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
;  FILE REFERENCE: PC006
;  CURRENT APPLICATION NUMBER: US/09/764,891
;  CURRENT FILING DATE:  2001-01-17
;  Prior application data removed - consult PALM or file wrapper
;  NUMBER OF SEQ ID NOS: 10231
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 810
;   LENGTH: 662
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: (321)
;   OTHER INFORMATION: n equals a,t,g, or c
US-09-764-891-810

  Query Match             24.7%;  Score 53.4;  DB 11;  Length 662;
  Best Local Similarity   63.8%;  Pred. No. 3.5e-07;
  Matches   81;  Conservative    0;  Mismatches   46;  Indels    0;  Gaps    0;

Qy         74 TCTCGAGGCAGCCCAGCCTCAACGCCTACAACTCACTGACAAGGTCGGGGCTGAAGCGTA 133
              |||| || |||  ||||  || |    |  | | ||  | ||| |||| || ||| | |
Db         28 TCTCCAGACAGAGCAGCTACACCAGTAATGGCACTCTTCCTAGGACGGGACTAAAGAGGA 87

Qy        134 CGCCCTCGCTAAAGCCGGACGTACCCCCCAAACCATCCTTTGCTCCCCTTTCCACATCCA 193
              |||| ||   ||| || ||||| || || || || |||||||| ||| |   || ||||
Db         88 CGCCGTCTTAAAAACCTGACGTGCCACCAAAGCCTTCCTTTGTTCCTCAAACCCCATCTG 147

Qy        194 TGAAGCC 200
              | |  ||
Db        148 TCAGACC 154


RESULT 12
US-10-027-632-166826/c
; Sequence 166826, Application US/10027632
; GENERAL INFORMATION:
;  APPLICANT: Wang, David G.
;  TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
;  TITLE OF INVENTION:  Polymorphisms in the Human Genome
;  FILE REFERENCE: 108827.129
;  CURRENT APPLICATION NUMBER: US/10/027,632
;  CURRENT FILING DATE:  2002-04-30
;  PRIOR APPLICATION NUMBER: US 60/218,006
;  PRIOR FILING DATE: 2000-07-12
;  PRIOR APPLICATION NUMBER: US 60/198,676
;  PRIOR FILING DATE: 2000-04-20
;  PRIOR APPLICATION NUMBER: US 60/193,483
;  PRIOR FILING DATE: 2000-03-29
;  PRIOR APPLICATION NUMBER: US 60/185,218
;  PRIOR FILING DATE: 2000-02-24
;  PRIOR APPLICATION NUMBER: US 60/167,363
;  PRIOR FILING DATE: 1999-11-23
;  PRIOR APPLICATION NUMBER: US 60/156,358
;  PRIOR FILING DATE: 1999-09-28
;  PRIOR APPLICATION NUMBER: US 60/146,002
;  PRIOR FILING DATE: 1999-08-09
;  NUMBER OF SEQ ID NOS: 325720
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 166826
;   LENGTH: 765
;   TYPE: DNA
;   ORGANISM: Human
US-10-027-632-166826

  Query Match             17.3%;  Score 37.4;  DB 13;  Length 765;
  Best Local Similarity   55.9%;  Pred. No. 0.036;
  Matches   71;  Conservative    0;  Mismatches   56;  Indels    0;  Gaps    0;

Qy         33 CCAGGTGCACAGCTCCCAGCCATCTGGCCAGGCCGTGACTGTCTCGAGGCAGCCCAGCCT 92
              || ||| | |||  | |  ||||||||||  ||    |||  |  |   | | || | |
Db        268 CCTGGTCCCCAGGCCGCCACCATCTGGCCGTGCACACACTCGCCTGGTCCTGGCCGGACC 209

Qy         93 CAACGCCTACAACTCACTGACAAGGTCGGGGCTGAAGCGTACGCCCTCGCTAAAGCCGGA 152
              | | |  |  | ||   |||||||  | || || |||  | | || |   | |||| |
Db        208 AGAGGGCGTCTGCACAGGTACAAGGTGGCGGGTGGAGCCCAGGACCCCTGGACAGCCAGG 149

Qy        153 CGTACCC 159
              |   |||
Db        148 CCATCCC 142


RESULT 13
US-09-554-000-7/c
; Sequence 7, Application US/09554000
; Patent No. US20020165364A1
; GENERAL INFORMATION:
;  APPLICANT: Tsien, Roger Y.
;  APPLICANT:  Miyawaki, Atsushi
;  TITLE OF INVENTION: FLUORESCENT PROTEIN SENSORS FOR
;  TITLE OF INVENTION:  DETECTION OF ANALYTES
;  FILE REFERENCE: 07257/042001
;  CURRENT APPLICATION NUMBER: US/09/554,000
;  CURRENT FILING DATE:  2000-04-20
;  PRIOR APPLICATION NUMBER: 08/818,252
;  PRIOR FILING DATE: 1997-03-14
;  NUMBER OF SEQ ID NOS: 56
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7
;   LENGTH: 1971
;   TYPE: DNA
;   ORGANISM: Aequorea victoria
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (0)...(1968)
US-09-554-000-7

  Query Match             16.4%;  Score 35.4;  DB 10;  Length 1971;
  Best Local Similarity   61.3%;  Pred. No. 0.17;
  Matches   57;  Conservative    0;  Mismatches   36;  Indels    0;  Gaps    0;

Qy          2 CGCCGCCCGCCCCGCAGAGGGTGGACTCCATCCAGGTGCACAGCTCCCAGCCATCTGGCC 61
              ||||| ||  | ||   ||| ||| | ||| || |||| ||||||||  ||| |    |
Db        112 CGCCGTCCAGCTCGACCAGGATGGGCACCACCCCGGTGAACAGCTCCTCGCCCTTGCTCA 53

Qy         62 AGGCCGTGACTGTCTCGAGGCAGCCCAGCCTCA 94
              | | | | | |   | ||   |||||||  ||
Db         52 CGTCGGCGGCGGCGCCCAGCAGGCCCAGCAGCA 20


RESULT 14
US-10-128-714-2578
; Sequence 2578, Application US/10128714
; Publication No. US20030119013A1
; GENERAL INFORMATION:
;  APPLICANT: Jiang, Bo
;  APPLICANT:  Hu, Wenqi
;  APPLICANT:  Tishkoff, Daniel
;  APPLICANT:  Zamudio, Carlos
;  APPLICANT:  Eroshkin, Alexey M
;  APPLICANT:  Lemieux, Sebastien M
;  TITLE OF INVENTION: Identification of Essential Genes in Aspergillus fumigatus an
;  TITLE OF INVENTION:  Methods of Use
;  FILE REFERENCE: 10182-018-999
;  CURRENT APPLICATION NUMBER: US/10/128,714
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;  CURRENT FILING DATE:  2002-04-23
;  PRIOR APPLICATION NUMBER: US 60/285,697
;  PRIOR FILING DATE: 2001-04-23
;  PRIOR APPLICATION NUMBER: US 60/287,066
;  PRIOR FILING DATE: 2001-04-27
;  PRIOR APPLICATION NUMBER: US 60/295,890
;  PRIOR FILING DATE: 2001-06-05
;  PRIOR APPLICATION NUMBER: US 60/303,899
;  PRIOR FILING DATE: 2001-07-09
;  PRIOR APPLICATION NUMBER: US 60/316,362
;  PRIOR FILING DATE: 2001-08-31
;  NUMBER OF SEQ ID NOS: 8603
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2578
;   LENGTH: 936
;   TYPE: DNA
;   ORGANISM: Aspergillus fumigatus
US-10-128-714-2578

  Query Match             16.3%;  Score 35.2;  DB 14;  Length 936;
  Best Local Similarity   55.8%;  Pred. No. 0.18;
  Matches   67;  Conservative    0;  Mismatches   53;  Indels    0;  Gaps    0;

Qy         86 CCAGCCTCAACGCCTACAACTCACTGACAAGGTCGGGGCTGAAGCGTACGCCCTCGCTAA 145
              ||| |  |||| | ||||| ||   ||  || | |  |  |||| | |          |
Db        152 CCACCAACAACAGCAACAACCCAGCAACCCGGACAGCTCCCAAGCCTCCTATTGTCTCCA 211

Qy        146 AGCCGGACGTACCCCCCAAACCATCCTTTGCTCCCCTTTCCACATCCATGAAGCCCAATG 205
              |||   | |||| | |||||||||   ||  ||   ||||| |||| |   ||| ||
Db        212 CGCCCACCCTACCAGCAAAACCATCCACCGCCTCCACCTCCACCTCCAACACCTCCACTG 271


RESULT 15
US-10-128-714-7578
; Sequence 7578, Application US/10128714
; Publication No. US20030119013A1
; GENERAL INFORMATION:
;  APPLICANT: Jiang, Bo
;  APPLICANT:  Hu, Wenqi
;  APPLICANT:  Tishkoff, Daniel
;  APPLICANT:  Zamudio, Carlos
;  APPLICANT:  Eroshkin, Alexey M
;  APPLICANT:  Lemieux, Sebastien M
;  TITLE OF INVENTION: Identification of Essential Genes in Aspergillus fumigatus and
;  TITLE OF INVENTION:  Methods of Use
;  FILE REFERENCE: 10182-018-999
;  CURRENT APPLICATION NUMBER: US/10/128,714
;  CURRENT FILING DATE:  2002-04-23
;  PRIOR APPLICATION NUMBER: US 60/285,697
;  PRIOR FILING DATE: 2001-04-23
;  PRIOR APPLICATION NUMBER: US 60/287,066
;  PRIOR FILING DATE: 2001-04-27
;  PRIOR APPLICATION NUMBER: US 60/295,890
;  PRIOR FILING DATE: 2001-06-05
;  PRIOR APPLICATION NUMBER: US 60/303,899
;  PRIOR FILING DATE: 2001-07-09
;  PRIOR APPLICATION NUMBER: US 60/316,362
;  PRIOR FILING DATE: 2001-08-31
;  NUMBER OF SEQ ID NOS: 8603
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7578
;   LENGTH: 936
;   TYPE: DNA
;   ORGANISM: Aspergillus fumigatus
US-10-128-714-7578

  Query Match             16.3%;  Score 35.2;  DB 14;  Length 936;
  Best Local Similarity   55.8%;  Pred. No. 0.18;
  Matches   67;  Conservative    0;  Mismatches   53;  Indels    0;  Gaps    0;

Qy         86 CCAGCCTCAACGCCTACAACTCACTGACAAGGTCGGGGCTGAAGCGTACGCCCTCGCTAA 145
              ||| |  |||| | ||||| ||   ||  || | |  |  |||| | |          |
Db        152 CCACCAACAACAGCAACAACCCAGCAACCCGGACAGCTCCCAAGCCTCCTATTGTCTCCA 211

Qy        146 AGCCGGACGTACCCCCCAAACCATCCTTTGCTCCCCTTTCCACATCCATGAAGCCCAATG 205
              |||   | |||| | |||||||||   ||  ||   ||||| |||| |   ||| ||
Db        212 CGCCCACCCTACCAGCAAAACCATCCACCGCCTCCACCTCCACCTCCAACACCTCCACTG 271


Search completed: September 30, 2003, 22:20:07
Job time : 63.2004 secs
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